GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 10:23:07 ; Search time 55.16 Seconds
(without alignments)
388.637 Million cell updates/sec

Title: US-09-155-327E-7
Perfect score: 1007
Sequence: 1 MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1007	100.0	193	20	AAY05530	Human Bcl-w protei
2	1002	99.5	193	19	AAW61392	Human bcl-y protei
3	1002	99.5	193	20	AAW97392	The human bcl-y pr
4	1000	99.3	193	18	AAW36047	Human bcl-w protei
5	1000	99.3	193	20	AAY05531	Mouse Bcl-w protei
6	1000	99.3	193	20	AAY05532	Human Bcl-w protei
7	997	99.0	192	20	AAW97394	Mammalian bcl-y pr
8	996	98.9	193	19	AAW61391	Rat bcl-y protein.
9	996	98.9	193	20	AAW97391	The rat bcl-y prot
10	991	98.4	192	20	AAW97393	Protein sequence o
11	958.5	95.2	192	20	AAY05533	Mouse Bcl-w protei
12	867	86.1	168	18	AAW36048	Mouse bcl-w protei
13	766	76.1	365	19	AAW59884	Amino acid sequenc
14	433.5	43.0	411	22	AAU00219	Bcl-Xl-DTR apoptos
15	428.5	42.6	233	16	AAR68887	Human thymus BCL-X
16	428.5	42.6	233	17	AAW05821	Bcl-XL protein. H
17	428.5	42.6	233	18	AAW31530	Human anti-apoptot
18	428.5	42.6	233	21	AAY83223	Bcl-x polypeptide.
19	428.5	42.6	233	21	AAY69969	Human Bcl-XL prote
20	428.5	42.6	233	22	AAG64262	Human Bcl-XL prote
21	428.5	42.6	233	22	AAB73303	Rat wild-type Bcl-
22	428.5	42.6	233	22	AAB50538	Human Bcl-xL prote
23	428.5	42.6	233	22	AAB47515	Protein encoded by
24	425	42.2	225	18	AAW19396	"Deprenyl" (RTM)-i
25	424.5	42.2	233	22	AAB73304	Mutant rat Bcl-xL
26	416.5	41.4	239	22	AAG64037	Human Bcl-2 protei
27	413	41.0	236	22	AAB35131	Murine Bcl-2. Mus
28	412.5	41.0	239	20	AAW87810	A human Bcl-2 prot
29	412.5	41.0	239	22	AAB74127	Human bcl-2. Homo
30	412.5	41.0	239	22	AAB35130	Human Bcl-2. Homo
31	410.5	40.8	239	9	AAP80987	Sequence of bcl-2-
32	410.5	40.8	239	14	AAR42312	Bcl-2 oncogene pro
33	410.5	40.8	239	16	AAR70331	Human bcl-2 protei
34	410.5	40.8	239	16	AAR71404	Human bcl-2 alpha
35	410.5	40.8	239	19	AAW40217	Human bcl-2. Homo
36	410.5	40.8	239	20	AAW87812	A human Bcl-2-alph
37	410.5	40.8	239	22	AAE08573	Human Bcl-2 protei
38	410.5	40.8	239	22	AAG64035	Human Bcl-2 protei
39	410.5	40.8	239	22	AAG64036	Human Bcl-2 protei
40	410.5	40.8	239	22	AAB74129	Human bcl-2alpha.
41	410.5	40.8	239	22	AAB48288	Human BCL-2 protei
42	410.5	40.8	239	22	AAB50537	Human Bcl-2 protei
43	410.5	40.8	272	19	AAY21120	Human bcl2 proto-o
44	410.5	40.8	485	22	AAU00222	LFn-Bcl-XL apoptos
45	409	40.6	232	17	AAW01019	Apoptosis-blocking

ALIGNMENTS

RESULT 1
AAY05530
ID AAY05530 standard; Protein; 193 AA.
XX
AC AAY05530;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human Bcl-w protein essential for spermatogenesis.
XX
KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
KW animal model.
XX
OS Homo sapiens.
XX
PN WO9913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU00764.
XX
PR 16-SEP-1997; 97AU-0009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
XX
DR WPI; 1999-243890/20.
DR N-PSDB; AAX25132.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w
XX
PS Claim 2; Page 33; 52pp; English.

```
XX
CC   The present sequence is human Bcl-w, a pro-survival member of the
CC   Bcl-2 family which is widely expressed and which is essential for
CC   spermatogenesis.  The invention relates generally to a method of
CC   treatment and to an animal model for the identification of
CC   molecules and genetic sequences useful for inducing or reducing
CC   fertility of male animals.  Methods are provided for the treatment
CC   of infertility, or for reducing fertility, by modulating
CC   spermatogenesis.  An animal model carries a mutation is at least
CC   one allele of the human or murine bcl-w gene (see AAX25132-35) or in
CC   a gene associated with bcl-w.  Such animals have disorganised
CC   seminferous tubules and are substantially infertile, but possess no
CC   other major abnormalities as determined by histological examination.
CC   They can be used to screen for therapeutic molecules including
CC   genetic sequences capable of inducing, enhancing or otherwise
CC   facilitating spermatogenesis in animals, or which can induce
CC   infertility.
XX
SQ   Sequence   193 AA;


  Query Match             100.0%;  Score 1007;  DB 20;  Length 193;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-103;
  Matches  193;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
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Db     121 qvqewmvayletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgaval 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 galvtvgaffask 193


RESULT   2
AAW61392
ID   AAW61392 standard; Protein; 193 AA.
XX
AC   AAW61392;
XX
DT   02-OCT-1998  (first entry)
XX
DE   Human bcl-y protein.
XX
KW   bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
XX
OS   Homo sapiens.
XX
PN   US5789201-A.
XX
PD   04-AUG-1998.
XX
PF   11-FEB-1997;   97US-0798897.
XX
PR   23-FEB-1996;   96US-0012201.
PR   11-FEB-1997;   97US-0798897.
XX
PA   (COCE-) COCENSYS INC.
XX
PI   Guastella J;
XX
DR   WPI; 1998-446079/38.
DR   N-PSDB; AAV28334.
XX
PT   Nucleic acids encoding B-cell lymphoma-y protein - useful for
PT   producing recombinant protein for use in treating uncontrolled cell
PT   growth e.g. cancers
XX
PS   Example; Column 17/18; 27pp; English.
XX
CC   The mammalian bcl-y protein is a member of the bcl-2 family, components
CC   in the cell death pathway.  The bcl-2 family have both apoptotic activity
CC   and the apoptosis blocking activity.  bcl-y falls in the apoptosis
CC   activity category.  The recombinant protein may be used to prevent
CC   uncontrolled cell growth, either by its direct administration to
CC   recombinant genetic constructs to increase its expression in vivo.  Also,
CC   antisense constructs can be used in disorders where prevention of cell
CC   death is desired.
XX
SQ   Sequence   193 AA;


  Query Match             99.5%;  Score 1002;  DB 19;  Length 193;
  Best Local Similarity   99.5%;  Pred. No. 9.3e-103;
  Matches  192;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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Db      61 fsdlaaqlhvtpgsaqqrftqvsdelfqgggpnwgrlvaffvfgaalcaesvnkemeplvg 120

Qy     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
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Db     121 qvqewmvayletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgaval 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 galvtvgaffask 193


RESULT   3
AAW97392
ID   AAW97392 standard; Protein; 193 AA.
XX
AC   AAW97392;
XX
DT   20-MAY-1999  (first entry)
XX
DE   The human bcl-y protein.
XX
KW   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW   multiple sclerosis; myocardial infarction; vitally induced cell death;
KW   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW   premature cell death; cell death stimulator; prolonged cell life span;
KW   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW   parasite.
XX
OS   Homo sapiens.
XX
PN   US5883229-A.
XX
PD   16-MAR-1999.
XX
PF   25-NOV-1997;   97US-0978523.
XX
PR   23-FEB-1996;   96US-0012201.
PR   11-FEB-1997;   97US-0798897.
PR   25-NOV-1997;   97US-0978523.
XX
PA   (COCE-) COCENSYS INC.
XX
PI   Guastella J;
XX
```

DR WPI; 1999-214150/18.
DR N-PSDB; AAX15946.
XX
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
PT for modulating programmed cell death
XX
PS Claim 1; Columns 17-18; 26pp; English.
XX
CC The present sequence represents human bcl-y protein (Hbcl-y). The
CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and
CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral
CC sclerosis- conditions where cells under go premature cell death as a
CC result of triggers which may or may not be apparent. They may also be
CC used in this way to develop cell lines which remain viable in culture for
CC an extended period. In contrast, if they act as cell death stimulators,
CC Rbcl-y and Hbcl-y may be used to treat conditions associated with
CC prolonged cell life span such as cancer (especially kaposi's sarcoma and
CC lung cancer) and auto/hyperimmune diseases. They may also be used to
CC cause cell death in, and hence control, parasites.
XX
SQ Sequence 193 AA;

Query Match 99.5%; Score 1002; DB 20; Length 193;
Best Local Similarity 99.5%; Pred. No. 9.3e-103;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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Qy     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
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Db     121 qvqewmvayletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgaval 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 galvtvgaffask 193
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RESULT 4
AAW36047
ID AAW36047 standard; Protein; 193 AA.
XX
AC AAW36047;
XX
DT 22-APR-1998 (first entry)
XX
DE Human bcl-w protein.
XX
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW diagnosis; degenerative disease.
XX
OS Homo sapiens.
XX
PN WO9735971-A1.
XX
PD 02-OCT-1997.
XX
PF 27-MAR-1997; 97WO-AU00199.
XX
PR 27-MAR-1996; 96AU-0008965.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Adams JM, Cory S, Gibson LM, Holmgreen SP;
XX
DR WPI; 1997-489635/45.
DR N-PSDB; AAT96577.
XX
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce
PT or inhibit cell survival, e.g. for treatment of cancer and
PT degenerative diseases
XX
PS Claim 6; Page 48; 86pp; English.
XX
CC This sequence represents a novel human protein, bcl-w, encoded by the
CC bcl-2 gene family and extracted from an adult brain library. This gene
CC promotes cell survival, so its modulation is useful in treatment of
CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,
CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,
CC ischaemia, human immunodeficiency virus infection or in cell transplants.
CC Up-regulation of the gene can also be used to modify cell lines cultured
CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
CC and to increase survival of primary explants during genetic modification.
CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,
CC antibody production or screening of potential modulators.
XX
SQ Sequence 193 AA;

Query Match 99.3%; Score 1000; DB 18; Length 193;
Best Local Similarity 99.0%; Pred. No. 1.6e-102;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
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Db       1 matpasapdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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Qy     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
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Db     121 qvqewmvayletrlvdwihssggwaeftalygdgaleearrlregnwasvrtvltgaval 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 galvtvgaffask 193
```

RESULT 5
AAY05531
ID AAY05531 standard; Protein; 193 AA.
XX
AC AAY05531;
XX
DT 05-JUL-1999 (first entry)
XX
DE Mouse Bcl-w protein essential for spermatogenesis.
XX
KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
KW animal model.
XX
OS Mus sp.
XX
PN WO9913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU00764.
XX
PR 16-SEP-1997; 97AU-0009228.
XX

```
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI   Adams J,  Cory S,  Gibson L,  Koentgen F,  Print C;
XX
DR   WPI; 1999-243890/20.
DR   N-PSDB; AAX25133.
XX
PT   An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT   protein associated with Bcl-w
XX
PS   Claim 2; Page 35; 52pp; English.
XX
CC   The present sequence is mouse Bcl-w, a pro-survival member of the
CC   Bcl-2 family which is widely expressed and which is essential for
CC   spermatogenesis.  The invention relates generally to a method of
CC   treatment and to an animal model for the identification of
CC   molecules and genetic sequences useful for inducing or reducing
CC   fertility of male animals.  Methods are provided for the treatment
CC   of infertility, or for reducing fertility, by modulating
CC   spermatogenesis.  An animal model carries a mutation is at least
CC   one allele of the human or murine bcl-w gene (see AAX25132-35) or in
CC   a gene associated with bcl-w.  Such animals have disorganised
CC   seminferous tubules and are substantially infertile, but possess no
CC   other major abnormalities as determined by histological examination.
CC   They can be used to screen for therapeutic molecules including
CC   genetic sequences capable of inducing, enhancing or otherwise
CC   facilitating spermatogenesis in animals, or which can induce
CC   infertility.
XX
SQ   Sequence   193 AA;


  Query Match             99.3%;  Score 1000;  DB 20;  Length 193;
  Best Local Similarity   99.0%;  Pred. No. 1.6e-102;
  Matches  191;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 matpastpdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 qvqdwmvayletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgaval 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 galvtvgaffask 193


RESULT   6
AAY05532
ID   AAY05532 standard; Protein; 193 AA.
XX
AC   AAY05532;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Human Bcl-w protein essential for spermatogenesis.
XX
KW   Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
KW   animal model.
XX
OS   Homo sapiens.
XX
PN   WO9913710-A1.
XX
PD   25-MAR-1999.
XX
PF   16-SEP-1998;   98WO-AU00764.
XX
PR   16-SEP-1997;   97AU-0009228.
XX
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI   Adams J,  Cory S,  Gibson L,  Koentgen F,  Print C;
XX
DR   WPI; 1999-243890/20.
DR   N-PSDB; AAX25134.
XX
PT   An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT   protein associated with Bcl-w
XX
PS   Disclosure; Page 37; 52pp; English.
XX
CC   The present sequence is described of a derivative of human Bcl-w
CC   (see also AAY05530), a pro-survival member of the Bcl-2 family that
CC   is widely expressed and which is essential for spermatogenesis.
CC   The invention relates generally to a method of treatment and to an
CC   animal model for the identification of molecules and genetic
CC   sequences useful for inducing or reducing fertility of male animals.
CC   Methods are provided for the treatment of infertility, or for
CC   reducing fertility, by modulating spermatogenesis.  An animal model
CC   carries a mutation is at least one allele of the human or murine
CC   bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w.
CC   Such animals have disorganised seminferous tubules and are
CC   substantially infertile, but possess no other major abnormalities
CC   as determined by histological examination.  They can be used to
CC   screen for therapeutic molecules including genetic sequences
CC   capable of inducing, enhancing or otherwise facilitating
CC   spermatogenesis in animals, or which can induce infertility.
XX
SQ   Sequence   193 AA;


  Query Match             99.3%;  Score 1000;  DB 20;  Length 193;
  Best Local Similarity   99.0%;  Pred. No. 1.6e-102;
  Matches  191;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 matpasapdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db      61 fsdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvafflfgaalcaesvnkemeplvg 120

Qy     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     121 qvqewmvayletrlvdwihssggwaeftalygdgaleearrlregnwasvrtvltgaval 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 galvtvgaffask 193


RESULT   7
AAW97394
ID   AAW97394 standard; Protein; 192 AA.
XX
AC   AAW97394;
XX
DT   20-MAY-1999  (first entry)
XX
DE   Mammalian bcl-y protein.
XX
KW   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW   multiple sclerosis; myocardial infarction; vitally induced cell death;
KW   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW   premature cell death; cell death stimulator; prolonged cell life span;
KW   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
```

```
KW   parasite.
XX
OS   Mammalia.
XX
PN   US5883229-A.
XX
PD   16-MAR-1999.
XX
PF   25-NOV-1997;   97US-0978523.
XX
PR   23-FEB-1996;   96US-0012201.
PR   11-FEB-1997;   97US-0798897.
PR   25-NOV-1997;   97US-0978523.
XX
PA   (COCE-) COCENSYS INC.
XX
PI   Guastella J;
XX
DR   WPI; 1999-214150/18.
XX
PT   Novel bcl-y homologues of the rat and human bcl-2 protein  - useful
PT   for modulating programmed cell death
XX
PS   Claim 2; Columns 19-22; 26pp; English.
XX
CC   The present sequence represents a mammalian bcy-1 protein.
CC   The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
CC   protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
CC   thought to be involved in programmed cell death (apoptosis and necrosis).
CC   Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
CC   with a disruption of the cell death pathway. If they act as cell death
CC   inhibitors, they may be used in therapies to treat subjects suffering
CC   from: strokes, head trauma, Alzheimer's Disease, neural and muscular
CC   degenerative diseases (especially multiple sclerosis), myocardial
CC   infarction, vitally induced cell death, aging, spinal cord injuries and
CC   amyotrophic lateral sclerosis- conditions where cells under go premature
CC   cell death as a result of triggers which may or may not be apparent.
CC   They may also be used in this way to develop cell lines which remain
CC   viable in culture for an extended period. In contrast, if they act as
CC   cell death stimulators, Rbcl-y and Hbcl-y may be used to treat
CC   conditions associated with prolonged cell life span such as cancer
CC   (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune
CC   diseases. They may also be used to cause cell death in, and hence
CC   control, parasites.
XX
SQ   Sequence   192 AA;

  Query Match             99.0%;  Score 997;  DB 20;  Length 192;
  Best Local Similarity   99.5%;  Pred. No. 3.3e-102;
  Matches  191;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
           |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db       1 atpasapdtralvedfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrtf 60

Qy      62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvgq 120

Qy     122 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 vqewmvayletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgavalg 180

Qy     182 ALVTVGAFFASK 193
           ||||||||||||
Db     181 alvtvgaffask 192


RESULT   8
AAW61391
ID   AAW61391 standard; Protein; 193 AA.
XX
AC   AAW61391;
XX
DT   02-OCT-1998  (first entry)
XX
DE   Rat bcl-y protein.
XX
KW   bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
OS   Rattus sp.
XX
PN   US5789201-A.
XX
PD   04-AUG-1998.
XX
PF   11-FEB-1997;   97US-0798897.
XX
PR   23-FEB-1996;   96US-0012201.
PR   11-FEB-1997;   97US-0798897.
XX
PA   (COCE-) COCENSYS INC.
XX
PI   Guastella J;
XX
DR   WPI; 1998-446079/38.
DR   N-PSDB; V283333.
XX
PT   Nucleic acids encoding B-cell lymphoma-y protein - useful for
PT   producing recombinant protein for use in treating uncontrolled cell
PT   growth e.g. cancers
XX
PS   Example; Fig 3A; 27pp; English.
XX
CC   The mammalian bcl-y protein is a member of the bcl-2 family, components
CC   in the cell death pathway.  The bcl-2 family have both apoptotic activity
CC   and the apoptosis blocking activity.  bcl-y falls in the apoptosis
CC   activity category.  The recombinant protein may be used to prevent
CC   uncontrolled cell growth, either by its direct administration to
CC   recombinant genetic constructs to increase its expression in vivo.  Also,
CC   antisense constructs can be used in disorders where prevention of cell
CC   death is desired.
XX
SQ   Sequence   193 AA;

  Query Match             98.9%;  Score 996;  DB 19;  Length 193;
  Best Local Similarity   98.4%;  Pred. No. 4.3e-102;
  Matches  190;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 matpastpdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 fsdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvg 120

Qy     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||:||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 qvqdwmvtyletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgaval 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 galvtvgaffask 193


RESULT   9
AAW97391
ID   AAW97391 standard; Protein; 193 AA.
XX
AC   AAW97391;
XX
DT   20-MAY-1999  (first entry)
XX
```

```
DE   The rat bcl-y protein.
XX
KW   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW   multiple sclerosis; myocardial infarction; vitally induced cell death;
KW   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW   premature cell death; cell death stimulator; prolonged cell life span;
KW   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW   parasite.
XX
OS   Rattus sp.
XX
PN   US5883229-A.
XX
PD   16-MAR-1999.
XX
PF   25-NOV-1997;   97US-0978523.
XX
PR   23-FEB-1996;   96US-0012201.
PR   11-FEB-1997;   97US-0798897.
PR   25-NOV-1997;   97US-0978523.
XX
PA   (COCE-) COCENSYS INC.
XX
PI   Guastella J;
XX
DR   WPI; 1999-214150/18.
DR   N-PSDB; AAX15945.
XX
PT   Novel bcl-y homologues of the rat and human bcl-2 protein  - useful
PT   for modulating programmed cell death
XX
PS   Disclosure; Columns 15-18; 26pp; English.
XX
CC   The present sequence represents rat bcl-y protein (Rbcl-y). The
CC   specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
CC   Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC   programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC   proteins may be used to treat conditions associated with a disruption of
CC   the cell death pathway. If they act as cell death inhibitors, they may be
CC   used in therapies to treat subjects suffering from: strokes, head trauma,
CC   Alzheimer's Disease, neural and muscular degenerative diseases
CC   (especially multiple sclerosis), myocardial infarction, vitally induced
CC   cell death, aging, spinal cord injuries and amyotrophic lateral
CC   sclerosis- conditions where cells under go premature cell death as a
CC   result of triggers which may or may not be apparent. They may also be
CC   used in this way to develop cell lines which remain viable in culture for
CC   an extended period. In contrast, if they act as cell death stimulators,
CC   Rbcl-y and Hbcl-y may be used to treat conditions associated with
CC   prolonged cell life span such as cancer (especially kaposi's sarcoma and
CC   lung cancer) and auto/hyperimmune diseases. They may also be used to
CC   cause cell death in, and hence control, parasites.
XX
SQ   Sequence   193 AA;


  Query Match             98.9%;  Score 996;  DB 20;  Length 193;
  Best Local Similarity   98.4%;  Pred. No. 4.3e-102;
  Matches  190;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 matpastpdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 fsdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvg 120

Qy     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||:||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 qvqdwmvtyletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgaval 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 galvtvgaffask 193


RESULT  10
AAW97393
ID   AAW97393 standard; Protein; 192 AA.
XX
AC   AAW97393;
XX
DT   20-MAY-1999  (first entry)
XX
DE   Protein sequence of the specification.
XX
KW   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW   multiple sclerosis; myocardial infarction; vitally induced cell death;
KW   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW   premature cell death; cell death stimulator; prolonged cell life span;
KW   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW   parasite.
XX
OS   Unidentified.
XX
PN   US5883229-A.
XX
PD   16-MAR-1999.
XX
PF   25-NOV-1997;   97US-0978523.
XX
PR   23-FEB-1996;   96US-0012201.
PR   11-FEB-1997;   97US-0798897.
PR   25-NOV-1997;   97US-0978523.
XX
PA   (COCE-) COCENSYS INC.
XX
PI   Guastella J;
XX
DR   WPI; 1999-214150/18.
XX
PT   Novel bcl-y homologues of the rat and human bcl-2 protein  - useful
PT   for modulating programmed cell death
XX
PS   Disclosure; Columns 19-20; 26pp; English.
XX
CC   The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
CC   protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
CC   thought to be involved in programmed cell death (apoptosis and necrosis).
CC   Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
CC   with a disruption of the cell death pathway. If they act as cell death
CC   inhibitors, they may be used in therapies to treat subjects suffering
CC   from: strokes, head trauma, Alzheimer's Disease, neural and muscular
CC   degenerative diseases (especially multiple sclerosis), myocardial
CC   infarction, vitally induced cell death, aging, spinal cord injuries and
CC   amyotrophic lateral sclerosis- conditions where cells under go premature
CC   cell death as a result of triggers which may or may not be apparent.
CC   They may also be used in this way to develop cell lines which remain
CC   viable in culture for an extended period. In contrast, if they act as
CC   cell death stimulators, Rbcl-y and Hbcl-y may be used to treat
CC   conditions associated with prolonged cell life span such as cancer
CC   (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune
CC   diseases. They may also be used to cause cell death in, and hence
CC   control, parasites.
XX
SQ   Sequence   192 AA;


  Query Match             98.4%;  Score 991;  DB 20;  Length 192;
  Best Local Similarity   98.4%;  Pred. No. 1.5e-101;
  Matches  189;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy       2 ATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
           ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 atpastpdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrtf 60

Qy      62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sdlaaqlhvtpgsaqqrftqvsdelfqgggpnwgrlvaffvfgaalcaesvnkemeplvgq 120

Qy     122 VQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
           ||:||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 vqdwmvtyletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgavalg 180

Qy     182 ALVTVGAFFASK 193
           ||||||||||||
Db     181 alvtvgaffask 192
```

RESULT 11
AAY05533
ID AAY05533 standard; Protein; 192 AA.
XX
AC AAY05533;
XX
DT 05-JUL-1999 (first entry)
XX
DE Mouse Bcl-w protein deritvative.
XX
KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
KW animal model.
XX
OS Mus sp.
XX
PN WO9913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU00764.
XX
PR 16-SEP-1997; 97AU-0009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
XX
DR WPI; 1999-243890/20.
DR N-PSDB; AAX25135.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w
XX
PS Disclosure; Page 39; 52pp; English.
XX
CC The present sequence is described of a derivative of mouse Bcl-w
CC (see also AAY05531), a pro-survival member of the Bcl-2 family that
CC is widely expressed and which is essential for spermatogenesis.
CC The derivative lacks the 24 N-terminal amino acids of Bcl-w.
CC The invention relates generally to a method of treatment and to an
CC animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male animals.
CC Methods are provided for the treatment of infertility, or for
CC reducing fertility, by modulating spermatogenesis. An animal model
CC carries a mutation is at least one allele of the human or murine
CC bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w.
CC Such animals have disorganised seminferous tubules and are
CC substantially infertile, but possess no other major abnormalities
CC as determined by histological examination. They can be used to
CC screen for therapeutic molecules including genetic sequences
CC capable of inducing, enhancing or otherwise facilitating
CC spermatogenesis in animals, or which can induce infertility.
XX
SQ Sequence 192 AA;

Query Match 95.2%; Score 958.5; DB 20; Length 192;
Best Local Similarity 94.8%; Pred. No. 6.1e-98;
Matches 183; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

```
Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           | |||| |||||||||||||:||||||||||||||||||||||||||||||||||||||
Db       1 mptpastpdtralvadfvgyrlrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 fsdlaaqlhvtpgsaqqrftqvsdelfqgggpnwgrlvaffvfgaalcaesvnkemeplvg 120

Qy     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||:|:|||||||||||||||||:||||||||||:|||||||||| | ||:||||||
Db     121 qvqdwivayletrladwihssggwadftalygdgaledarrlregnwa-vstvvtgaval 179

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     180 galvtvgaffask 192
```

RESULT 12
AAW36048
ID AAW36048 standard; Protein; 168 AA.
XX
AC AAW36048;
XX
DT 22-APR-1998 (first entry)
XX
DE Mouse bcl-w protein.
XX
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW diagnosis; degenerative disease.
XX
OS Mus sp.
XX
PN WO9735971-A1.
XX
PD 02-OCT-1997.
XX
PF 27-MAR-1997; 97WO-AU00199.
XX
PR 27-MAR-1996; 96AU-0008965.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Adams JM, Cory S, Gibson LM, Holmgreen SP;
XX
DR WPI; 1997-489635/45.
DR N-PSDB; AAT96578.
XX
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce
PT or inhibit cell survival, e.g. for treatment of cancer and
PT degenerative diseases
XX
PS Claim 6; Page 50-51; 86pp; English.
XX
CC This sequence represents a novel protein, bcl-w, encoded by the mouse
CC bcl-2 gene family. This gene promotes cell survival, so its modulation
CC is useful in treatment of cancer or auto-immune diseases, degenerative
CC diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular
CC degeneration, hypoxia, ischaemia, human immunodeficiency virus infection
CC or in cell transplants. Up-regulation of the gene can also be used to
CC modify cell lines cultured in vivo, e.g. to develop new lines, to
CC facilitate isolation of hybridomas and to increase survival of primary
CC explants during genetic modification. It can be used to produce
CC recombinant Bcl-w for therapy, diagnosis, antibody production or
CC screening of potential modulators.
XX
SQ Sequence 168 AA;

Query Match 86.1%; Score 867; DB 18; Length 168;

```
  Best Local Similarity   95.8%;  Pred. No. 7e-88;
  Matches  161;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           | |||| |||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db       1 mptpastpdtralvadfvgyrlrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 fsdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvg 120

Qy     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWA 168
           |||:|:|||||||||||||||:||||||||||:||||||||||
Db     121 qvqdwivayletrladwihssggwadftalygdgaledarrlregnwa 168


RESULT  13
AAW59884
ID   AAW59884 standard; Protein; 365 AA.
XX
AC   AAW59884;
XX
DT   20-NOV-1998  (first entry)
XX
DE   Amino acid sequence of the cDNA clone Bcl-like (HAICH29).
XX
KW   Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
KW   immunological disorder; autoimmune disease; anti-infectious agent.
XX
OS   Homo sapiens.
XX
PN   WO9831800-A2.
XX
PD   23-JUL-1998.
XX
PF   21-JAN-1998;   98WO-US00960.
XX
PR   21-JAN-1997;   97US-0034205.
PR   21-JAN-1997;   97US-0034204.
XX
PA   (AUCK-) AUCKLAND UNISERVICES LTD.
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Feng P,  Gentz RL,  Krissansen GW,  Ni J,  Rosen CA;
PI   Su JY;
XX
DR   WPI; 1998-414099/35.
DR   N-PSDB; AAV41925.
XX
PT   New isolated polynucleotides and encoded polypeptides - used to
PT   develop products for treating e.g. inflammatory diseases,
PT   infections, immunological disorders, autoimmune diseases, allergies
PT   or tumours
XX
PS   Claim 1; Fig 12A-12D; 120pp; English.
XX
CC   This is the amino acid sequence of the cDNA clone Bcl-like (HAICH29),
CC   used in the method of the invention.  The products of the clone can be
CC   used for treating conditions associated with abnormal expression of
CC   the polypeptides.  They can be used for e.g. treating chronic
CC   inflammatory diseases, immunological disorders, autoimmune diseases,
CC   inflammatory diseases, various allergies, and as anti-infectious agents.
CC   The products can also be used for detection and diagnosis.
XX
SQ   Sequence   365 AA;


  Query Match             76.1%;  Score 766;  DB 19;  Length 365;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-76;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1 matpasapdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 fsdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvg 120

Qy     121 QVQEWMVAYLETRLADWIHSSGGW 144
           ||||||||||||||||||||||||
Db     121 qvqewmvayletrladwihssggw 144


RESULT  14
AAU00219
ID   AAU00219 standard; Protein; 411 AA.
XX
AC   AAU00219;
XX
DT   31-MAY-2001  (first entry)
XX
DE   Bcl-Xl-DTR apoptosis-modifying fusion protein.
XX
KW   Human; Bcl-Xl-DTR; apoptosis; cancer; spinal muscular atrophy;
KW   diphtheria toxin receptor binding domain; DTR; neoplasm; tumour;
KW   hyper-proliferation; Alzheimer's disease; neurodegenerative disorder;
KW   transient ischaemic neuronal injury; stroke; spinal cord injury;
KW   Huntington's disease.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Corynebacterium diptheriae.
OS   Chimeric - Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          3..12
FT                   /note= "10x histidine tag"
FT   Domain          21..253
FT                   /note= "Bcl-Xl amino acids 1 to 233"
FT   Region          254..259
FT                   /note= "Linker amino acids, linking Bcl-Xl to diphtheria
FT                          toxin receptor binding domain (DTR)"
FT   Domain          260..411
FT                   /note= "DTR, diphtheria toxin receptor binding domain"
XX
PN   WO200112661-A2.
XX
PD   22-FEB-2001.
XX
PF   15-AUG-2000; 2000WO-US22293.
XX
PR   16-AUG-1999;   99US-0149220.
XX
PA   (HARD ) HARVARD COLLEGE.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Youle RJ,  Liu X,  Collier RJ;
XX
DR   WPI; 2001-218343/22.
DR   N-PSDB; AAS00247.
XX
PT   Novel fusion protein for modifying apoptosis in target cell and
PT   reducing apoptosis after transient ischaemic neuronal injury, has two
PT   domains which targets protein to a cell and modifies apoptotic response
PT   of cell  -
XX
PS   Claim 4; Page 56-57; 65pp; English.
XX
CC   The sequence represents the amino acid sequence of Bcl-Xl-DTR apoptosis-
CC   modifying fusion protein comprising Bcl-Xl sequence fused via a short
CC   linker to diphtheria toxin receptor binding domain (DTR). The functional
CC   apoptosis-modifying fusion protein is capable of binding a target cell
CC   and integrating into or crossing a cellular membrane of the target cell.
CC   comprising at least two domains, one of which targets the fusion protein
CC   to the target cell and another of which modifies an apoptotic response of
CC   the target cell. The fusion protein is useful for modifying (inhibiting
```

```
CC   or enhancing) apoptosis in a target cell, such as neuron, lymphocyte,
CC   cancer, neoplasm, macrophage, epithelial, stem, tumour or hyper-
CC   proliferative cell or an adipocyte. It is also useful for reducing
CC   apoptosis in a subject after transient ischaemic neuronal injury,
CC   especially spinal cord injury. The fusion protein may be used to treat
CC   various diseases and injury conditions through inhibition or enhancement
CC   of apoptotic cellular response, including neurodegenerative disorders
CC   such as Alzheimer's disease, Huntington's disease, spinal muscular
CC   atrophy, stroke episodes and unregulated cell growth as in tumours and
CC   various cancers. The apoptosis-modifying fusion protein can be delivered
CC   effectively throughout the body and targeted to selective tissue and
CC   cells.
XX
SQ   Sequence   411 AA;

  Query Match             43.0%;  Score 433.5;  DB 22;  Length 411;
  Best Local Similarity   39.9%;  Pred. No. 2.5e-39;
  Matches   93;  Conservative   26;  Mismatches   63;  Indels   51;  Gaps    4;

Qy      11 RALVADFVGYKLRQKGY--------------------------VCGAGP----GEGPAA 39
           | || ||: ||| ||||                                    |     : ||
Db      26 relvvdflsyklsqkgyswsqfsdveenrteapegtesemetpsaingnpswhladspav 85

Qy      40 D-----------------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
           :                  : ||:| |||||| |:|| |||| :|||:|||:| | | |
Db      86 ngatahsssldarevipmaavkqalreagdefelryrrafsdltsqlhitpgtayqsfeq 145

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
           | :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||  :
Db     146 vvnelfrdgvnwgrivaffsfggalcvesvdkemqvlvsriaawmatylndhlepwiqen 205

Qy     142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGALVTVGAFFAS 192
           |||  |  |||: |  |:|: :|    |      : | | ||:| :  |: |:
Db     206 ggwdtfvelygnnaaaesrkgqerfnrwfltgmtvagvvllgslfsrkaysaa 258


RESULT  15
AAR68887
ID   AAR68887 standard; Protein; 233 AA.
XX
AC   AAR68887;
XX
DT   10-AUG-1995  (first entry)
XX
DE   Human thymus BCL-XL.
XX
KW   BCL-XL; apoptosis; cell death; cancer; neurodegenerative disease;
KW   autoimmune disease; Parkinson disease; amylotrophic lateral sclerosis;
KW   multiple sclerosis.
XX
OS   Homo sapiens.
XX
PN   WO9500642-A.
XX
PD   05-JAN-1995.
XX
PF   22-JUN-1994;   94WO-US07089.
XX
PR   22-JUN-1993;   93US-0081448.
XX
PA   (ARCH-) ARCH DEV CORP.
PA   (UNMI ) UNIV MICHIGAN.
XX
PI   Boise LH,  Nunez G,  Thompson CB;
XX
DR   WPI; 1995-052079/07.
DR   N-PSDB; AAQ81698.
XX
PT   New poly-nucleotide encoding new poly-peptide(s) that modify
PT   apoptosis - and related vectors, recombinant cells and
PT   antibodies, useful in assay and for control of cell death in e.g.
PT   neuronal cells, lymphocytes and cancers
XX
PS   Claim 3; Page 94; 127pp; English.
XX
CC   This protein may be expressed recombinantly, particularly with pcmV
CC   plasmids as vectors for expression in mammalian cell cultures.  The
CC   protein has particular application in cancer cells (failure of
CC   programmed cell death (PCD)) or neurodegenerative and autoimmune
CC   diseases (premature PCD), e.g. Parkinson's disease, amylotrophic
CC   lateral sclerosis and multiple sclerosis.
XX
SQ   Sequence   233 AA;

  Query Match             42.6%;  Score 428.5;  DB 16;  Length 233;
  Best Local Similarity   41.3%;  Pred. No. 4.1e-39;
  Matches   93;  Conservative   22;  Mismatches   57;  Indels   53;  Gaps    4;

Qy      11 RALVADFVGYKLRQKGY-----------------------------------------V 28
           | || ||: ||| ||||                                         |
Db       6 relvvdflsyklsqkgyswsqfsdveenrteapegtesemetpsaingnpswhladspav 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
            ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 nga-tghsssldarevipmaavkqalreagdefelryrrafsdltsqlhitpgtayqsfe 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 qvvnelfrdgvnwgrivaffsfggalcvesvdkemqvlvsriaawmatylndhlepwiqe 184

Qy     141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           :|||  |  |||: |  |:|: :|    |      : | | ||:|
Db     185 nggwdtfvelygnnaaaesrkgqerfnrwfltgmtvagvvllgsl 229


Search completed: June 10, 2002, 10:25:47
Job time: 160 sec
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 10:23:32 ; Search time 28.15 Seconds
(without alignments)
658.801 Million cell updates/sec

Title: US-09-155-327E-7
Perfect score: 1007
Sequence: 1 MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	428.5	42.6	233	2	I49056	bcl-x long - mouse
2	428.5	42.6	233	2	B47537	apoptosis regulato
3	424.5	42.2	233	2	S51761	BCL-X protein - ra
4	423.5	42.1	233	2	A37332	transforming prote
5	414	41.1	232	2	S24390	transforming prote
6	412.5	41.0	239	1	TVHUA1	transforming prote
7	412	40.9	236	2	I67432	BCL-2 - rat (fragm
8	407	40.4	236	2	I53744	gene bcl-2 protein
9	406	40.3	236	1	TVMSA1	transforming prote
10	404.5	40.2	233	2	I67431	BCL-X-Long - rat
11	403	40.0	236	2	JC7383	B-cell lymphoma 2
12	378	37.5	190	2	A47537	apoptosis regulato
13	377.5	37.5	214	2	I49057	bcl-x transmembran
14	375.5	37.3	227	2	JE0203	apoptosis regulato
15	356	35.4	216	2	B37332	transforming prote
16	349.5	34.7	199	1	TVMSB1	transforming prote
17	346	34.4	205	1	TVHUB1	transforming prote
18	277.5	27.6	154	2	I58194	gene bcl-2 protein
19	182	18.1	170	2	I49055	bcl-x short - mous
20	176	17.5	211	2	S58873	Bak protein - huma
21	174	17.3	176	2	I67435	gene bcl-xshort pr
22	173	17.2	211	2	S58875	cdn-2 protein - hu
23	157.5	15.6	192	2	D47538	bcl-2-associated p
24	153	15.2	192	2	A47538	bcl-2-associated p
25	150	14.9	261	2	H88578	protein ced-9 [imp
26	150	14.9	280	2	A53189	apoptosis suppress
27	149.5	14.8	133	2	I53295	bcl-2-associated p
28	146.5	14.5	179	2	JC7255	Bax-delta protein
29	146.5	14.5	218	2	B47538	bcl-2-associated p
30	143	14.2	177	2	S54778	NR-13 protein - qu
31	141	14.0	255	2	JC7567	Mcl-1a protein - z
32	137.5	13.7	143	2	I38921	bcl-2-associated p
33	118	11.7	175	2	I39055	Bcl-2 related - hu
34	112	11.1	350	2	A47476	BCL2 homolog MCL1
35	105	10.4	172	2	I49449	hemopoietic-specif
36	91.5	9.1	301	2	T36534	probable lipase/es
37	89	8.8	185	2	B83217	hypothetical prote
38	87	8.6	3433	1	GNWVKV	genome polyprotein
39	85	8.4	270	2	AI2598	dihydrodipicolinat
40	85	8.4	279	2	B97381	dihydrodipicolinat
41	84.5	8.4	358	1	AJLCQB	glutamate--ammonia
42	83	8.2	417	2	T39939	DNA binding protei
43	82.5	8.2	1440	1	GNWVJF	genome polyprotein
44	82.5	8.2	3432	1	GNWVJE	genome polyprotein
45	81.5	8.1	354	2	S52040	Gln 1.1 protein -

ALIGNMENTS

RESULT 1
I49056
bcl-x long - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C;Accession: I49056; S52866
R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes
A;Reference number: I49055; MUID:95052604
A;Accession: I49056
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-233 <RES>
A;Cross-references: EMBL:U10101; NID:g506647; PIDN:AAA82173.1; PID:g506648
R;Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
submitted to the EMBL Data Library, November 1994
A;Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line th
A;Reference number: S52866
A;Accession: S52866
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-233 <KAM>
A;Cross-references: EMBL:X83574; NID:g695622; PIDN:CAA58557.1; PID:g695623
C;Superfamily: bcl transforming protein

Query Match 42.6%; Score 428.5; DB 2; Length 233;
Best Local Similarity 41.3%; Pred. No. 2.9e-32;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

```
Qy      11 RALVADFVGYKLRQKGY----------------------------------------V 28
           | || ||: ||| ||||                                         |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy     141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           :||| | |||: | |:|: :|    |      : | | ||:|
Db     185 NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229
```

RESULT 2
B47537
apoptosis regulator bcl-xL - human
N;Alternate names: bcl-2-related protein

```
N;Contains: apoptosis regulator bcl-xS
C;Species: Homo sapiens (man)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C;Accession: B47537; C47537
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74, 597-608, 1993
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A;Reference number: A47537; MUID:93364977
A;Accession: B47537
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-233 <BOI>
A;Cross-references: GB:L20121; NID:g510900; PIDN:CAA80661.1; PID:g510901
A;Accession: C47537
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-69,'G',71-125,189-233 <BO2>
A;Cross-references: GB:L20122; NID:g623236; PIDN:CAA80662.1; PID:g623237
C;Genetics:
A;Gene: GDB:BCL2L
A;Cross-references: GDB:228079
C;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; apoptosis
F;1-233/Product: apoptosis regulator bcl-xL #status predicted <MAT>
F;1-125,189-233/Product: apoptosis regulator bcl-xS #status predicted <MA2>


  Query Match             42.6%;  Score 428.5;  DB 2;  Length 233;
  Best Local Similarity   40.6%;  Pred. No. 2.9e-32;
  Matches   91;  Conservative   23;  Mismatches   59;  Indels   51;  Gaps    4;

Qy      11 RALVADFVGYKLRQKGY--------------------------VCGAGP----GEGPAA 39
           | || ||: ||| ||||                                      |      : ||
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65

Qy      40 D------------------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
           :                  : ||:| |||||| |:|| |||| :|||:|||:| | | |
Db      66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 125

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
           | :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||  :
Db     126 VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQEN 185

Qy     142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           |||  |  |||: |  |:|: :|    |      : | | ||:|
Db     186 GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT   3
S51761
BCL-X protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 02-Mar-2001
C;Accession: S51761; S51762
R;Michaelidis, T.M.
submitted to the EMBL Data Library, November 1994
A;Reference number: S51761
A;Accession: S51761
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <MIC>
A;Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57886.1; PID:g607177
A;Experimental source: embryonic; brain
A;Accession: S51762
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125,189-233 <MI2>
A;Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57887.1; PID:g607178
A;Experimental source: embryonic; brain
A;Note: smaller form due to splicing
C;Genetics:
A;Introns: 125/3
C;Superfamily: bcl transforming protein


  Query Match             42.2%;  Score 424.5;  DB 2;  Length 233;
  Best Local Similarity   41.3%;  Pred. No. 6.8e-32;
  Matches   92;  Conservative   22;  Mismatches   56;  Indels   53;  Gaps    4;

Qy      13 LVADFVGYKLRQKGY----------------------------------------VCG 30
           || ||: ||| ||||                                        | |
Db       8 LVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAVNG 67

Qy      31 AGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQV 82
           |  |  : |          : ||:| |||||| |:|| |||| :|||:|||:| | | ||
Db      68 A-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQV 126

Qy      83 SDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSG 142
           :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||  :|
Db     127 VNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENG 186

Qy     143 GWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           ||  |  |||: |  |:|: :|    |      : | | ||:|
Db     187 GWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT   4
A37332
transforming protein (bcl-2-alpha) - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 23-Feb-1997
C;Accession: A37332; S35453
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a va
A;Reference number: A37332; MUID:92375724
A;Accession: A37332
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-233 <EGU>
A;Cross-references: EMBL:D11381
C;Genetics:
A;Introns: 189/3
C;Superfamily: bcl transforming protein
C;Keywords: mitochondrion; transforming protein; transmembrane protein


  Query Match             42.1%;  Score 423.5;  DB 2;  Length 233;
  Best Local Similarity   38.0%;  Pred. No. 8.4e-32;
  Matches   87;  Conservative   32;  Mismatches   61;  Indels   49;  Gaps    4;

Qy       9 DTRALVADFVGYKLRQKGYVCGAG-------PGEGPAADP-------------------- 41
           | | :|  :: ||| |:||   ||       |   ||| |
Db      10 DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPEPPGSA 69

Qy      42 -----------------LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSD 84
                           :| |:| |||||  |::| |: :: |||:|| :|  ||  | :
Db      70 AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE 129

Qy      85 ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGW 144
           |||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   | :||  :|||
Db     130 ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW 189

Qy     145 AEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
             |  |||:      | | : :| |::|:|:  | :|| :|:||:   |
Db     190 DAFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK 233


RESULT   5
S24390
transforming protein (Bcl-2) homolog - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S24390
R;Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.
Biochim. Biophys. Acta 1132, 109-113, 1992
```

A;Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue
A;Reference number: S24390; MUID:92379084
A;Accession: S24390
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-232 <CAZ>
A;Cross-references: EMBL:Z11961; NID:g62969; PIDN:CAA78018.1; PID:g62970
C;Superfamily: bcl transforming protein
C;Keywords: mitochondrion; transmembrane protein

Query Match 41.1%; Score 414; DB 2; Length 232;
Best Local Similarity 37.7%; Pred. No. 6.3e-31;
Matches 86; Conservative 32; Mismatches 62; Indels 48; Gaps 4;

```
Qy       9 DTRALVADFVGYKLRQKGYVCGAG-------PGEGPAADP---------------------- 41
           | | :|  :: ||| |:||   ||        |   ||| |
Db      10 DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPSPPARL 69

Qy      42 ---------------LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
                          :| |:| |||||  |::| |: :: |||:|| :|  ||  | :|
Db      70 LLVRCPRLRGCAAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTATGRFVAVVEE 129

Qy      86 LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWA 145
           ||: | || |:|||| ||  :| ||||:|| |||  :  ||  ||   | :||  :|||
Db     130 LFRDGVNWVRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGWD 189

Qy     146 EFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
             |  |||:      | | : :| |::|:|:  | :|| :|:||:   |
Db     190 AFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK 232
```

RESULT 6
TVHUA1
transforming protein bcl-2, splice form alpha - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change 15-Oct-1999
C;Accession: C37332; A29409; S02452; A24428; A27622; B27622
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
A;Reference number: A37332; MUID:92375724
A;Accession: C37332
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-239 <EGU>
A;Note: this report is a correction
R;Tsujimoto, Y.; Croce, C.M.
Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
A;Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene
A;Reference number: A29409; MUID:86259760
A;Accession: A29409
A;Molecule type: mRNA
A;Residues: 1-95,'A',97-109,'G',111-236,'S',238-239 <TSU>
A;Cross-references: GB:M13994; NID:g179366; PIDN:AAA51813.1; PID:g179367
A;Note: this sequence has been corrected in reference A37332
R;Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeye
EMBO J. 7, 123-131, 1988
A;Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2
A;Reference number: S02452; MUID:88196071
A;Accession: S02452
A;Molecule type: mRNA
A;Residues: 1-239 <SET>
R;Cleary, M.L.; Smith, S.D.; Sklar, J.
Cell 47, 19-28, 1986
A;Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglo
A;Reference number: A24428; MUID:87002488
A;Accession: A24428
A;Molecule type: mRNA
A;Residues: 1-58,'T',60-116,'R',118-239 <CLE>
A;Cross-references: GB:M14745; NID:g179370; PIDN:AAA35591.1; PID:g179371
R;Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakhshi, A.
Oncogene Res. 2, 263-275, 1988

A;Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphom
A;Reference number: A27622; MUID:88217344
A;Accession: A27622
A;Molecule type: mRNA
A;Residues: 1-58,'T',60-239 <HUA>
A;Accession: B27622
A;Molecule type: DNA
A;Residues: 1-6,'S',8-58,'T',60-128,'C',130-239 <HUA2>
A;Note: the sequence was determined from the germline gene
C;Comment: Constitutive expression of BCL2 following t(14:18) chromosomal translocati
C;Genetics:
A;Gene: GDB:BCL2
A;Cross-references: GDB:119031; OMIM:151430
A;Map position: 18q21.3-18q21.3
C;Function:
A;Description: blocks apoptosis in hematopoietic cells
C;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; pr

Query Match 41.0%; Score 412.5; DB 1; Length 239;
Best Local Similarity 37.0%; Pred. No. 9e-31;
Matches 87; Conservative 34; Mismatches 59; Indels 55; Gaps 5;

```
Qy       9 DTRALVADFVGYKLRQKGYVCGAG-------------------PGE-------------- 35
           | | :|  :: ||| |:||   ||                    ||
Db      10 DNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAPAPGIFSSQPGHTPHPAASRDPVART 69

Qy      36 -------------GPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQR 78
                        |||  |    :|  :| |||:|  |:|| |:::::|||:|| :|: |
Db      70 SPLQTPAAPGAAAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGR 129

Qy      79 FTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWI 138
           |  | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||
Db     130 FATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWI 189

Qy     139 HSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
             :|||  |  |||       | | : :| |::|:|: |: :|| :|:||:   |
Db     190 QDNGGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 239
```

RESULT 7
I67432
BCL-2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: I67432
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: eq
onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
A;Reference number: I53295; MUID:95129487
A;Accession: I67432
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-236 <RES>
A;Cross-references: EMBL:U34964; NID:g1004378; PIDN:AAA77687.1; PID:g1004379
C;Superfamily: bcl transforming protein

Query Match 40.9%; Score 412; DB 2; Length 236;
Best Local Similarity 36.2%; Pred. No. 9.9e-31;
Matches 84; Conservative 34; Mismatches 62; Indels 52; Gaps 3;

```
Qy       9 DTRALVADFVGYKLRQKGY---------------------------------------- 27
           | | :|  :: ||| |:||
Db      10 DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRRAPTPGIFSFQPESNRTPAVHRDTAART 69

Qy      28 ------VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                 |  |||   |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db      70 SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
```

```
          | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||  :
Db    130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMYPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy    142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
          |||  |  |||       | | : :| |::|:|: |: :|| :|:||:   |
Db    190 GGWDAFVELYG----PSMRPLFDFSWQSLKTLLSLAL-VGACITLGAYLGHK 236


RESULT   8
I53744
gene bcl-2 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C;Accession: I53744
R;Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.
Gene 140, 291-292, 1994
A;Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.
A;Reference number: I53744; MUID:94193015
A;Accession: I53744
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-236 <RES>
A;Cross-references: GB:L14680; NID:g408946; PIDN:AAA53662.1; PID:g408947
C;Genetics:
A;Gene: bcl-2
C;Superfamily: bcl transforming protein


  Query Match             40.4%;  Score 407;  DB 2;  Length 236;
  Best Local Similarity   35.8%;  Pred. No. 2.9e-30;
  Matches   83;  Conservative   34;  Mismatches   63;  Indels   52;  Gaps    3;

Qy      9 DTRALVADFVGYKLRQKGY----------------------------------------- 27
          | | :|  :: ||| |:||
Db     10 DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRAAPTPGIFSFQPESNRTPAVHRDTAART 69

Qy     28 ------VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                |  |||    |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db     70 SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy     82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
          | :|||: | ||||:|||| ||  :|  |||:|| |||  :  ||  ||   |  ||  :
Db    130 VVEELFRDGVNWGRIVAFFEFGGVMCVGSVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy    142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
          |||  |  |||       | | : :| |::|:|: |: :|| :|:||:   |
Db    190 GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236


RESULT   9
TVMSA1
transforming protein bcl-2-alpha - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999
C;Accession: A25960; E37332
R;Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
Cell 49, 455-463, 1987
A;Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homol
A;Reference number: A90893; MUID:87187643
A;Accession: A25960
A;Molecule type: DNA
A;Residues: 1-236 <NEG>
A;Cross-references: GB:L31532; GB:M16506; NID:g468336; PIDN:AAA37282.1; PID:g387109
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
A;Reference number: A37332; MUID:92375724
A;Accession: E37332
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 1-33,'E',34-220,'AL',223-236 <EGU>
C;Genetics:
A;Gene: BCL2
A;Introns: 192/3
C;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane


  Query Match             40.3%;  Score 406;  DB 1;  Length 236;
  Best Local Similarity   37.1%;  Pred. No. 3.6e-30;
  Matches   86;  Conservative   33;  Mismatches   61;  Indels   52;  Gaps    5;

Qy      9 DTRALVADFVGYKLRQKGYVCGAG------------PG---------------------- 34
          | | :|  :: ||| |:||   ||             ||
Db     10 DNREIVMKYIHYKLSQRGYEWDAGDADAAPLGAAPTPGIFSFQPESNPMPAVHREMAART 69

Qy     35 ---------EGPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                   |||  |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db     70 SPLRPLVATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy     82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
          | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||  :
Db    130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy    142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
          |||  |  |||       | | : :| |::|:|:    :|| :|:||:   |
Db    190 GGWDAFVELYG----PSMRPLFDFSWLSLKTLLS-LPWVGACITLGAYLGHK 236


RESULT  10
I67431
BCL-X-Long - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: I67431
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: eq
onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
A;Reference number: I53295; MUID:95129487
A;Accession: I67431
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-233 <RES>
A;Cross-references: EMBL:U34963; NID:g1004376; PIDN:AAA77686.1; PID:g1004377
C;Superfamily: bcl transforming protein


  Query Match             40.2%;  Score 404.5;  DB 2;  Length 233;
  Best Local Similarity   39.6%;  Pred. No. 4.8e-30;
  Matches   89;  Conservative   22;  Mismatches   61;  Indels   53;  Gaps    4;

Qy     11 RALVADFVGYKLRQKGY-----------------------------------------V 28
          | || ||: ||| ||||                                         |
Db      6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAV 65

Qy     29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
           ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:  | |
Db     66 NGA-TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTVYQSFE 124

Qy     81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
          || :|||: | ||||:||   || ||| |||:|||: || ::  ||  ||   |  ||
Db    125 QVVNELFRDGVNWGRIVASSSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy    141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
          :|||  |  |||:    |:|: :|    |      : | | ||:|
Db    185 NGGWDTFVDLYGNNTAPESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT  11
JC7383
B-cell lymphoma 2 protein - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 08-Dec-2000
C;Accession: JC7383
R;Tomicic, M.T.; Christmann, M.; Kaina, B.
```

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Biochem. Biophys. Res. Commun. 275, 899-903, 2000
A;Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
A;Reference number: JC7383
A;Contents: Ovary
A;Accession: JC7383
A;Molecule type: mRNA
A;Residues: 1-236 <TOM>
A;Cross-references: GB:AJ271720
C;Comment: This protein has anti-apoptotic function, and supports cell survival.
C;Genetics:
A;Gene: bcl-2
C;Superfamily: bcl transforming protein
C;Keywords: B-cell lymphoma; ovary


  Query Match             40.0%;  Score 403;  DB 2;  Length 236;
  Best Local Similarity   35.3%;  Pred. No. 6.7e-30;
  Matches   82;  Conservative   34;  Mismatches   64;  Indels   52;  Gaps    3;

Qy       9 DTRALVADFVGYKLRQKGY---------------------------------------- 27
           | | :|  :: ||| |:||
Db      10 DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART 69

Qy      28 ------VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                 |   ||   |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db      70 SPLRPIVATTGPTLSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
           | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||  :
Db     130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy     142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
           |||  |  |||       | | : :| |::|:|: |: :|| :|:| :   |
Db     190 GGWDAFVELYG----PSVRPLFDFSWLSLKTLLSLAL-VGACITLGTYLGHK 236


RESULT  12
A47537
apoptosis regulator bcl-x - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999
C;Accession: A47537
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74, 597-608, 1993
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A;Reference number: A47537; MUID:93364977
A;Accession: A47537
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-190 <BOI>
A;Cross-references: GB:Z23110; GB:L20120; NID:g510898; PIDN:CAA80657.1; PID:g510899
C;Superfamily: bcl transforming protein


  Query Match             37.5%;  Score 378;  DB 2;  Length 190;
  Best Local Similarity   43.8%;  Pred. No. 1.1e-27;
  Matches   81;  Conservative   14;  Mismatches   44;  Indels   46;  Gaps    3;

Qy      11 RALVADFVGYKLRQKGY----------------------VCGAGPGEGP---------- 37
           | || ||| ||| |:|:                      |    |   |
Db       6 RELVIDFVSYKLSQRGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT 65

Qy      38 ------------AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
                       |  : ||:| |||||| |:|| |||| :|||:|||:| | | || :|
Db      66 VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE 125

Qy      86 LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWA 145
           ||  | ||||:|||| || ||| |||:|||  |||::  ||  ||   |  ||  :|||
Db     126 LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWV 185

Qy     146 EFTAL 150
             |||
Db     186 R-TAL 189


RESULT  13
I49057
bcl-x transmembrane deleted - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C;Accession: I49057
R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes
A;Reference number: I49055; MUID:95052604
A;Accession: I49057
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-214 <RES>
A;Cross-references: EMBL:U10102; NID:g506649; PIDN:AAA82174.1; PID:g506650
C;Genetics:
A;Gene: bcl-x-long
C;Superfamily: bcl transforming protein


  Query Match             37.5%;  Score 377.5;  DB 2;  Length 214;
  Best Local Similarity   42.8%;  Pred. No. 1.4e-27;
  Matches   80;  Conservative   16;  Mismatches   40;  Indels   51;  Gaps    3;

Qy      11 RALVADFVGYKLRQKGY----------------------------------------V 28
           | || ||: ||| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy     141 SGGWAEF 147
           :|||  |
Db     185 NGGWDTF 191


RESULT  14
JE0203
apoptosis regulator bcl-x isoform - human
N;Alternate names: h-bcl-xbeta
C;Species: Homo sapiens (man)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 16-Jul-1999
C;Accession: JE0203
R;Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler, E.
Biochem. Biophys. Res. Commun. 248, 147-152, 1998
A;Title: Identification of a human cDNA encoding a novel bcl-x isoform.
A;Reference number: JE0203; MUID:98340865
A;Accession: JE0203
A;Molecule type: mRNA
A;Residues: 1-227 <BAN>
A;Cross-references: GB:U72398; NID:g1622940; PIDN:AAB17354.1; PID:g1622941
C;Genetics:
A;Gene: bcl-x
A;Map position: 20
C;Superfamily: bcl transforming protein


  Query Match             37.3%;  Score 375.5;  DB 2;  Length 227;
  Best Local Similarity   40.8%;  Pred. No. 2.3e-27;
  Matches   82;  Conservative   18;  Mismatches   50;  Indels   51;  Gaps    3;

Qy      11 RALVADFVGYKLRQKGY----------------------------------------V 28
           | || ||: ||| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
```

```
          ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db     66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy     81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
          || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db    125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE 184

Qy    141 SGGWAEFTALYGDGALEEARR 161
          :|||     |    :|   :|
Db    185 NGGWVRTKPLVCPFSLASGQR 205


RESULT  15
B37332
transforming protein (bcl-2-beta) - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 24-Apr-1998
C;Accession: B37332; S35452
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
A;Reference number: A37332; MUID:92375724
A;Accession: B37332
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-216 <EGU>
A;Cross-references: EMBL:D11381; EMBL:D11382
C;Superfamily: bcl transforming protein


  Query Match             35.4%;  Score 356;  DB 2;  Length 216;
  Best Local Similarity   38.4%;  Pred. No. 1.4e-25;
  Matches   71;  Conservative   21;  Mismatches   49;  Indels   44;  Gaps    2;

Qy      9 DTRALVADFVGYKLRQKGYVCGAG-------PGEGPAADP-------------------- 41
          | | :|  :: ||| |:||   ||       |   ||| |
Db     10 DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPEPPGSA 69

Qy     42 -----------------LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSD 84
                           :| |:| |||||  |::| |: :: |||:|| :|  ||  | :
Db     70 AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE 129

Qy     85 ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGW 144
          |||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   | :||  :|||
Db    130 ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW 189

Qy    145 AEFTA 149
              |
Db    190 VRACA 194


Search completed: June 10, 2002, 10:26:22
Job time: 170 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 10:26:27 ; Search time 15.84 Seconds
(without alignments)
471.772 Million cell updates/sec

Title: US-09-155-327E-7
Perfect score: 1007
Sequence: 1 MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1007	100.0	193	1	BCLW_HUMAN	Q92843 homo sapien
2	1000	99.3	193	1	BCLW_MOUSE	P70345 mus musculu
3	646.5	64.2	228	1	AR1_XENLA	Q91827 xenopus lae
4	432.5	42.9	229	1	BCLX_CHICK	Q07816 gallus gall
5	431.5	42.9	233	1	BCLX_PIG	O77737 sus scrofa
6	428.5	42.6	233	1	BCLX_HUMAN	Q07817 homo sapien
7	428.5	42.6	233	1	BCLX_MOUSE	Q64373 mus musculu
8	428.5	42.6	233	1	BCLX_RAT	P53563 rattus norv
9	423.5	42.1	233	1	BCL2_CHICK	Q00709 gallus gall
10	416.5	41.4	229	1	BCL2_BOVIN	O02718 bos taurus
11	414	41.1	236	1	BCL2_RAT	P49950 rattus norv
12	413	41.0	236	1	BCL2_MOUSE	P10417 mus musculu
13	412.5	41.0	239	1	BCL2_HUMAN	P10415 homo sapien
14	403	40.0	236	1	BCL2_CRILO	Q9jjv8 cricetulus
15	371	36.8	204	1	AR11_XENLA	Q91828 xenopus lae
16	177.5	17.6	208	1	BAK_MOUSE	O08734 mus musculu
17	176	17.5	211	1	BAK_HUMAN	Q16611 homo sapien
18	173	17.2	211	1	BAK2_HUMAN	Q13014 homo sapien
19	155.5	15.4	192	1	BAXA_MOUSE	Q07813 mus musculu
20	154.5	15.3	192	1	BAXA_RAT	Q63690 rattus norv
21	153	15.2	192	1	BAXA_HUMAN	Q07812 homo sapien
22	150	14.9	280	1	CED9_CAEEL	P41958 caenorhabdi
23	147	14.6	192	1	BAXA_BOVIN	O02703 bos taurus
24	146.5	14.5	218	1	BAXB_HUMAN	Q07814 homo sapien
25	143	14.2	177	1	NR13_COTJA	Q90343 coturnix co
26	137.5	13.7	143	1	BAXD_HUMAN	P55269 homo sapien
27	136.5	13.6	271	1	CED9_CAEBR	P41957 caenorhabdi
28	118	11.7	175	1	BFL1_HUMAN	Q16548 homo sapien
29	112	11.1	350	1	MCL1_HUMAN	Q07820 homo sapien
30	105	10.4	172	1	BFL1_MOUSE	Q07440 mus musculu
31	99.5	9.9	179	1	EAR_ASFM2	Q07819 african swi
32	98.5	9.8	179	1	EAR_ASFB7	P42485 african swi
33	98.5	9.8	179	1	EAR_ASFE4	Q07818 african swi
34	88.5	8.8	658	1	SQHC_BRAJA	P54924 bradyrhizob
35	87	8.6	3433	1	POLG_KUNJM	P14335 k genome po
36	85.5	8.5	358	1	GLNA_LACSA	P23712 lactuca sat
37	82.5	8.2	1440	1	POLG_JAEVN	P14403 j genome po
38	82.5	8.2	3432	1	POLG_JAEVJ	P32886 j genome po
39	81	8.0	396	1	PORA_PYRFU	Q51804 pyrococcus
40	79	7.8	541	1	FTCD_RAT	O88618 rattus norv
41	79	7.8	3430	1	POLG_WNV	P06935 w genome po
42	78.5	7.8	886	1	A4_DROME	P14599 drosophila
43	78	7.7	509	1	TSSP_MOUSE	Q9qxe5 mus musculu
44	77.5	7.7	454	1	YB48_MYCTU	O06548 mycobacteri
45	77.5	7.7	454	1	YJ45_MYCTU	P95269 mycobacteri

ALIGNMENTS

RESULT 1
BCLW_HUMAN
ID BCLW_HUMAN STANDARD; PRT; 193 AA.
AC Q92843;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apoptosis regulator Bcl-W.
GN BCL2L2 OR BCLW OR KIAA0271.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358615; PubMed=8761287;
RA Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;
RT "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
RL Oncogene 13:665-675(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97191544; PubMed=9039502;
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. VI.
RT The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
RT analysis of cDNA clones from cell line KG-1 and brain.";
RL DNA Res. 3:321-329(1996).
CC -!- FUNCTION: PROMOTES CELL SURVIVAL.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND
CC IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,
CC AND SALIVARY GLAND.
CC -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC FUNCTION.
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC --

CC --
DR EMBL; U59747; AAB09055.1; -.
DR EMBL; D87461; BAA19666.1; -.
DR HSSP; Q07817; 1MAZ.
DR MIM; 601931; -.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR003093; BH4.

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DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis.
FT   DOMAIN        9     29       BH4.
FT   DOMAIN       85    104       BH1.
FT   DOMAIN      136    151       BH2.
SQ   SEQUENCE   193 AA;  20774 MW;  3792243A50281761 CRC64;
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  Query Match             100.0%;  Score 1007;  DB 1;  Length 193;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-83;
  Matches  193;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 GALVTVGAFFASK 193
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RESULT   2
BCLW_MOUSE
ID   BCLW_MOUSE     STANDARD;      PRT;   193 AA.
AC   P70345;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Apoptosis regulator Bcl-W.
GN   BCL2L2 OR BCLW.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96358615; PubMed=8761287;
RA   Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,
RA   Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;
RT   "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
RL   Oncogene 13:665-675(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/10J;
RX   MEDLINE=98160183; PubMed=9500547;
RA   Ross A.J., Waymire K.G., Moss J.E., Parlow A.F., Skinner M.K.,
RA   Russell L.D., Macgregor G.R.;
RT   "Testicular degeneration in Bclw-deficient mice.";
RL   Nat. Genet. 18:251-256(1998).
CC   -!- FUNCTION: PROMOTES CELL SURVIVAL.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND
CC       IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,
CC       AND SALIVARY GLAND.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION.
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U59746; AAB09056.1; -.
DR   EMBL; AF030769; AAB86430.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   MGD; MGI:108052; Bcl2l2.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis.
FT   DOMAIN        9     29       BH4.
FT   DOMAIN       85    104       BH1.
FT   DOMAIN      136    151       BH2.
SQ   SEQUENCE   193 AA;  20790 MW;  36CA185F5945DFB4 CRC64;
```

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  Query Match             99.3%;  Score 1000;  DB 1;  Length 193;
  Best Local Similarity   99.0%;  Pred. No. 1e-82;
  Matches  191;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 GALVTVGAFFASK 193
```

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RESULT   3
AR1_XENLA
ID   AR1_XENLA      STANDARD;      PRT;   228 AA.
AC   Q91827;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Apoptosis regulator R1 (XR1) (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Head;
```

```
RX   MEDLINE=95331613; PubMed=7607538;
RA   Cruz-Reyes J., Tata J.R.;
RT   "Cloning, characterization and expression of two Xenopus bcl-2-like
RT   cell-survival genes.";
RL   Gene 158:171-179(1995).
CC   -!- FUNCTION: COULD BE THE HOMOLOG OF MAMMALIAN BCL-W.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC   -!- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
CC       BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND
CC       ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X82462; CAA57845.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
KW   Apoptosis; Transmembrane.
FT   NON_TER       1      1
FT   DOMAIN      120    139       BH1.
FT   DOMAIN      171    186       BH2.
FT   TRANSMEM    207    227       POTENTIAL.
SQ   SEQUENCE   228 AA;  25068 MW;  C499D449A585F8A9 CRC64;


  Query Match             64.2%;  Score 646.5;  DB 1;  Length 228;
  Best Local Similarity   67.9%;  Pred. No. 5.7e-51;
  Matches  125;  Conservative   21;  Mismatches   35;  Indels    3;  Gaps    1;

Qy      10 TRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLH 69
           :|||| | | ||| |:  |       | |:  || |||||||||| |||: ||::: |:|
Db      48 SRALVEDLVRYKLCQRSLV---PEPSGAASCALHSAMRAAGDEFEERFRQAFSEISTQIH 104

Qy      70 VTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAY 129
           ||||:|  || :|:  ||||| ||||:||||||||||||||||| ||: ::|:||| |
Db     105 VTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDWMVTY 164

Qy     130 LETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAF 189
           ||| | ||| |:||  |  ||||||:||||| |||||||::||||||||||||:||||
Db     165 LETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGALMTVGAL 224

Qy     190 FASK 193
           ||||
Db     225 FASK 228


RESULT   4
BCLX_CHICK
ID   BCLX_CHICK     STANDARD;      PRT;   229 AA.
AC   Q07816; Q98908;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Apoptosis regulator Bcl-X.
GN   BCL2L1 OR BCLX OR BCL-X.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A. (SHORT FORM).
RX   MEDLINE=93364977; PubMed=8358789;
RA   Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA   Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT   "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT   of apoptotic cell death.";
RL   Cell 74:597-608(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (LONG FORM).
RC   STRAIN=HUBBARD WHITE MOUNTAIN; TISSUE=Testis;
RX   MEDLINE=97264485; PubMed=9110311;
RA   Vilagrasa X., Mezquita C., Mezquita J.;
RT   "Differential expression of bcl-2 and bcl-x during chicken
RT   spermatogenesis.";
RL   Mol. Reprod. Dev. 47:26-29(1997).
CC   -!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC       FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT
CC       ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC       ENVELOPE (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC       SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID
CC       DEVELOPMENT.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC       APOPTOTIC ACTIVITY (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Z23110; CAA80657.1; -.
DR   EMBL; U26645; AAB07677.1; -.
DR   PIR; A47537; A47537.
DR   HSSP; P53563; 1AF3.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Transmembrane; Alternative splicing.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       82     96       BH3.
FT   DOMAIN      125    144       BH1.
FT   DOMAIN      176    191       BH2.
FT   TRANSMEM    206    223       POTENTIAL.
FT   VARSPLIC    185    229       ERFVDLYGNNAAAELRKGQETFNKWLLTGATVAGVLLLGSL
FT                                LSRK -> VRTALP (IN SHORT ISOFORM).
SQ   SEQUENCE   229 AA;  25733 MW;  A97D3A4D04C0E9DA CRC64;
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  Query Match             42.9%;  Score 432.5;  DB 1;  Length 229;
  Best Local Similarity   41.7%;  Pred. No. 8.4e-32;
  Matches   95;  Conservative   22;  Mismatches   62;  Indels   49;  Gaps    4;

Qy      11 RALVADFVGYKLRQKGY----------------------VCGAGPGEGP---------- 37
           | || ||| ||| |:|:                      |    |   |
Db       6 RELVIDFVSYKLSQRGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT 65

Qy      38 ------------AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
                       |  : ||:| |||||| |:|| |||| :|||:|||:| | | || :|
Db      66 VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE 125

Qy      86 LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWA 145
           ||  | ||||:|||| || ||| |||:|||  |||::  ||  ||   |  ||  :|||
Db     126 LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWE 185

Qy     146 EFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
            |  |||: |   |  ||:|     : :||||   | |: :|:  : |
Db     186 RFVDLYGNNA---AAELRKGQETFNKWLLTGATVAGVLL-LGSLLSRK 229


RESULT   5
BCLX_PIG
ID   BCLX_PIG       STANDARD;      PRT;   233 AA.
AC   O77737;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Apoptosis regulator Bcl-x.
GN   BCL2L1 OR BLC2L OR BCLX.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT   "Expression of apoptosis-associated genes in hibernating and stunned
RT   myocardium of pig.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC       caspases (By similarity). Appears to regulate cell death by
CC       blocking the volatage-dependent anion channnel (VDAC) by binding
CC       to it and preventing the release of the caspase activator,
CC       cytochrome c, from the mitochondrial membrane.
CC   -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC       similarity). Heterodimerization with BAX does not seem to be
CC       required for anti-apoptotic activity (By similarity).
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC       ENVELOPE (BY SIMILARITY).
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC       The BH1 and BH2 domains are required for both heterodimerization
CC       with other Bcl2 family members and for repression of cell death.
CC   -!- PTM: Proteolytically cleaved by caspases during apoptosis (By
CC       similarity). The cleaved protein, lacking the BH4 domain, has pro-
CC       apoptotic activity (By similarity).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AJ001203; CAA04597.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Mitochondrion; Transmembrane.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       86    100       BH3.
FT   DOMAIN      129    148       BH1.
FT   DOMAIN      180    195       BH2.
FT   TRANSMEM    210    226       POTENTIAL.
SQ   SEQUENCE   233 AA;  26061 MW;  18BF6FA0441912B2 CRC64;


  Query Match             42.9%;  Score 431.5;  DB 1;  Length 233;
  Best Local Similarity   41.8%;  Pred. No. 1.1e-31;
  Matches   94;  Conservative   21;  Mismatches   57;  Indels   53;  Gaps    4;

Qy      11 RALVADFVGYKLRQKGY-----------------------------------------V 28
           | || ||: ||| ||||                                         |
Db       6 RELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVLNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQE 184

Qy     141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           :|||  |  |||: |  |:|: :|    |       | | | ||:|
Db     185 NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTLAGVVLLGSL 229


RESULT   6
BCLX_HUMAN
ID   BCLX_HUMAN     STANDARD;      PRT;   233 AA.
AC   Q07817; Q92976;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Apoptosis regulator Bcl-x.
GN   BCL2L1 OR BCL2L OR BCLX.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RX   MEDLINE=93364977; PubMed=8358789;
RA   Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA   Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT   "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT   of apoptotic cell death.";
RL   Cell 74:597-608(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM BETA).
RA   Inohara N., Ohta S.;
RL   Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.
RX   MEDLINE=95372373; PubMed=7644501;
RA   Sedlak T.W., Oltvai Z.N., Yang E., Wang K., Boise L.H., Thompson C.B.,
RA   Korsmeyer S.J.;
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RT   "Multiple Bcl-2 family members demonstrate selective dimerizations
RT   with Bax.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).
RN   [4]
RP   MUTAGENESIS OF BH1 AND BH2 DOMAINS.
RX   MEDLINE=96170038; PubMed=8596636;
RA   Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,
RA   Korsmeyer S.J.;
RT   "Bax-independent inhibition of apoptosis by Bcl-XL.";
RL   Nature 379:554-556(1996).
RN   [5]
RP   STRUCTURE BY NMR OF 1-209.
RX   MEDLINE=97172562; PubMed=9020082;
RA   Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E.,
RA   Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
RA   Thompson C.B., Fesik S.W.;
RT   "Structure of Bcl-xL-Bak peptide complex: recognition between
RT   regulators of apoptosis.";
RL   Science 275:983-986(1997).
RN   [6]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.
RX   MEDLINE=96256675; PubMed=8692274;
RA   Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,
RA   Yoon H.S., Nettesheim D., Chang B.S., Thompson C.B., Wong S.L.,
RA   Ng S.L., Fesik S.W.;
RT   "X-ray and NMR structure of human Bcl-xL, an inhibitor of programmed
RT   cell death.";
RL   Nature 381:335-341(1996).
RN   [7]
RP   CLEAVAGE BY CASPASES, AND MUTAGENESIS OF ASP-61.
RX   MEDLINE=98118550; PubMed=9435230;
RA   Clem R.J., Cheng E.H.-Y., Karp C.L., Kirsch D.G., Ueno K.,
RA   Takahashi A., Kastan M.B., Griffin D.E., Earnshaw W.C., Veliuona M.A.,
RA   Hardwick J.M.;
RT   "Modulation of cell death bx Bcl-xL through caspase interaction.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).
CC   -!- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC       caspases (By similarity). Appears to regulate cell death by
CC       blocking the volatage-dependent anion channnel (VDAC) by binding
CC       to it and preventing the release of the caspase activator,
CC       cytochrome c, from the mitochondrial membrane. The Bcl-x(S)
CC       isoform promotes apoptosis.
CC   -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2.
CC       Heterodimerization with BAX does not seem to be required for anti-
CC       apoptotic activity.
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC       ENVELOPE (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S)
CC       AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS
CC       THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING
CC       LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING
CC       LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC       The BH1 and BH2 domains are required for both heterodimerization
CC       with other Bcl2 family members and for repression of cell death.
CC   -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC       cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC       activity.
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Z23116; CAA80662.1; -.
DR   EMBL; Z23115; CAA80661.1; -.
DR   EMBL; U72398; AAB17354.1; -.
DR   PDB; 1BXL; 29-OCT-97.
DR   PDB; 1LXL; 21-APR-97.
DR   PDB; 1MAZ; 21-APR-97.
DR   MIM; 600039; -.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
KW   3D-structure.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       86    100       BH3.
FT   DOMAIN      129    148       BH1.
FT   DOMAIN      180    195       BH2.
FT   TRANSMEM    210    226       POTENTIAL.
FT   SITE         61     61       CLEAVAGE BY CASPASE-1.
FT   VARSPLIC    126    188       MISSING (IN ISOFORM BCL-X(S)).
FT   VARSPLIC    189    233       DTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
FT                                FSRK -> VRTKPLVCPFSLASGQRSPTALLLYLFLLCWVI
FT                                VGDVDS (IN ISOFORM BCL-X(BETA)).
FT   MUTAGEN      61     61       D->A: NO CLEAVAGE BY CASPASE-1 NOR BY
FT                                CASPASE-3.
FT   MUTAGEN      131    133      FRD->VRA: NO HETERODIMERIZATION WITH BAX.
FT   MUTAGEN      135    137      VNW->AIL: LOSS OF ANTI-APOPTOTIC
FT                                ACTIVITY.
FT   MUTAGEN      138    140      GRI->ELN: LOSS OF ANTI-APOPTOTIC
FT                                ACTIVITY.
FT   MUTAGEN      138    138      G->A: NO HETERODIMERIZATION WITH BAX.
FT   MUTAGEN      148    148      G->E: NO HETERODIMERIZATION WITH BAX.
FT   MUTAGEN      156    156      D->A: NO EFECT ON CASPASE-1 CLEAVAGE.
FT   MUTAGEN      176    176      D->A: NO EFECT ON CASPASE-1 CLEAVAGE.
FT   MUTAGEN      188    189      WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY
FT                                BY ABOUT HALF.
FT   MUTAGEN      189    189      D->A: NO EFECT ON CASPASE-1 CLEAVAGE.
FT   CONFLICT      70     70      G -> A (IN REF. 1; CAA80661).
SQ   SEQUENCE   233 AA;  26049 MW;  E09D3CDD851AE9BE CRC64;


  Query Match             42.6%;  Score 428.5;  DB 1;  Length 233;
  Best Local Similarity   41.3%;  Pred. No. 2e-31;
  Matches   93;  Conservative   22;  Mismatches   57;  Indels   53;  Gaps    4;

Qy      11 RALVADFVGYKLRQKGY----------------------------------------V 28
           | || ||: ||| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE 184

Qy     141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           :|||  |  |||: |  |:|: :|    |       : | | ||:|
Db     185 NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT   7
BCLX_MOUSE
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ID   BCLX_MOUSE     STANDARD;      PRT;   233 AA.
AC   Q64373; Q60657; Q60658; Q61338;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Apoptosis regulator Bcl-x.
GN   BCL2L1 OR BCL2L OR BCLX.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=2A4B;
RA   Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;
RL   Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=95331139; PubMed=7607090;
RA   Gonzalez-Garcia M., Perez-Ballestero R., Ding L., Duan L., Boise L.H.,
RA   Thompson C.B., Nunez G.;
RT   "bcl-XL is the major bcl-x mRNA form expressed during murine
RT   development and its product localizes to mitochondria.";
RL   Development 120:3033-3042(1994).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS X(L); X(S) AND X(DELTA-TM)).
RC   TISSUE=Pre-B cell;
RX   MEDLINE=95052604; PubMed=7963517;
RA   Fang W., Rivard J.J., Mueller D.L., Behrens T.W.;
RT   "Cloning and molecular characterization of mouse bcl-x in B and T
RT   lymphocytes.";
RL   J. Immunol. 153:4388-4398(1994).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM X(BETA)).
RC   STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX   MEDLINE=98051053; PubMed=9390687;
RA   Yang X.-F., Weber G.F., Cantor H.;
RT   "A novel Bcl-x isoform connected to the T cell receptor regulates
RT   apoptosis in T cells.";
RL   Immunity 7:629-639(1997).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97289584; PubMed=9144489;
RA   Grillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N.,
RA   Ohta S., Seldin M.F., Nunez G.;
RT   "Genomic organization, promoter region analysis, and chromosome
RT   localization of the mouse bcl-x gene.";
RL   J. Immunol. 158:4750-4757(1997).
CC   -!- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC       caspases (By similarity). Appears to regulate cell death by
CC       blocking the volatage-dependent anion channnel (VDAC) by binding
CC       to it and preventing the release of the caspase activator,
CC       cytochrome c, from the mitochondrial membrane. The Bcl-x(S)
CC       isoform promotes apoptosis.
CC   -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC       similarity). Heterodimerization with BAX does not seem to be
CC       required for anti-apoptotic activity (By similarity).
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC       ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELTA-TM).
CC   -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; BCX-X(L) (SHOWN HERE), BCL-X(S),
CC       BCL-X(BETA) AND BCL-X(DELTA-TM); ARE PRODUCED BY ALTERNATIVE
CC       SPLICING.
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN THE
CC       BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA-
CC       TM) EXPRESSION IS ENHANCED IN B AND T LYMPHOCYTES THAT HAVE BEEN
CC       ACTIVATED.
CC   -!- DEVELOPMENTAL STAGE: BCL-X(BETA)IS EXPRESSED IN BOTH EMBRYONAL AND
CC       POSTNATAL TISSUES, WHEREAS BCL-X(L) IS PREDOMINANTLY FOUND IN
CC       POSTNATAL TISSUES.
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC       The BH1 and BH2 domains are required for both heterodimerization
CC       with other Bcl2 family members and for repression of cell death.
CC   -!- PTM: Proteolytically cleaved by caspases during apoptosis (By
CC       similarity). The cleaved protein, lacking the BH4 domain, has pro-
CC       apoptotic activity (By similarity).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X83574; CAA58557.1; -.
DR   EMBL; L35049; AAA51039.1; -.
DR   EMBL; L35048; AAA51040.1; -.
DR   EMBL; U10102; AAA82174.1; -.
DR   EMBL; U10101; AAA82173.1; -.
DR   EMBL; U10100; AAA82172.1; -.
DR   EMBL; U51279; AAC53460.1; -.
DR   EMBL; U78031; AAB96881.1; -.
DR   EMBL; U78030; AAB96881.1; JOINED.
DR   HSSP; P53563; 1AF3.
DR   MGD; MGI:88139; Bcl2l.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       86    100       BH3.
FT   DOMAIN      129    148       BH1.
FT   DOMAIN      180    195       BH2.
FT   TRANSMEM    210    226       POTENTIAL.
FT   VARSPLIC    126    188       MISSING (IN ISOFORM BCL-X(S)).
FT   VARSPLIC    189    233       DTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
FT                                FSRK -> VRTTPLVCPPLACVSLLCEHP (IN ISOFORM
FT                                BCL-X(BETA)).
FT   VARSPLIC    194    233       LYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSLFSRK
FT                                -> GHDCGWCGSAGLTLQSEVTRH (IN ISOFORM BCL-
FT                                X(DELTA-TM)).
SQ   SEQUENCE   233 AA;  26132 MW;  24D2AC79887E072E CRC64;


  Query Match             42.6%;  Score 428.5;  DB 1;  Length 233;
  Best Local Similarity   41.3%;  Pred. No. 2e-31;
  Matches   93;  Conservative   22;  Mismatches   57;  Indels   53;  Gaps    4;

Qy      11 RALVADFVGYKLRQKGY----------------------------------------V 28
           | || ||: ||| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
              ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184
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Qy     141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           :|||  |  |||: |  |:|: :|    |      : | | ||:|
Db     185 NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT   8
BCLX_RAT
ID   BCLX_RAT       STANDARD;      PRT;   233 AA.
AC   P53563; Q62678; P70614; P70613; Q62836; Q64087; Q64128;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Apoptosis regulator Bcl-x.
GN   BCL2L1 OR BLC2L OR BCLX.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RC   TISSUE=Brain;
RA   Michaelidis T.M.;
RL   Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Wesselingh S.L., David G.L., Choi S., Veliuona M., Hardwick J.M.;
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
RC   TISSUE=Thymus;
RX   MEDLINE=96278736; PubMed=8662675;
RA   Shiraiwa N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Ohta S.;
RT   "An additional form of rat Bcl-x, Bcl-xbeta, generated by an
RT   unspliced RNA, promotes apoptosis in promyeloid cells.";
RL   J. Biol. Chem. 271:13258-13265(1996).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Ovary;
RX   MEDLINE=95129487; PubMed=7828536;
RA   Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
RT   "Expression of members of the bcl-2 gene family in the immature rat
RT   ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT   cell apoptosis is associated with decreased bax and constitutive
RT   bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
RL   Endocrinology 136:232-241(1995).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX   MEDLINE=98010630; PubMed=9346936;
RA   Aritomi M., Kunishima N., Inohara N., Ishibashi Y., Ohta S.,
RA   Morikawa K.;
RT   "Crystal structure of rat Bcl-xL. Implications for the function of
RT   the Bcl-2 protein family.";
RL   J. Biol. Chem. 272:27886-27892(1997).
CC   -!- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC       caspases (By similarity). Appears to regulate cell death by
CC       blocking the volatage-dependent anion channnel (VDAC) by binding
CC       to it and preventing the release of the caspase activator,
CC       cytochrome c, from the mitochondrial membrane. The Bcl-x(S) and
CC       Bcl-x(beta) isoforms promote apoptosis.
CC   -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC       similarity). Heterodimerization with BAX does not seem to be
CC       required for anti-apoptotic activity (By similarity).
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC       ENVELOPE (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S)
CC       AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS
CC       SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE
CC       OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT
CC       DETECTABLE LEVEL OF BCL-X(S).
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC       The BH1 and BH2 domains are required for both heterodimerization
CC       with other Bcl2 family members and for repression of cell death.
CC   -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC       cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC       activity (By similarity).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X82537; CAA57886.1; -.
DR   EMBL; X82537; CAA57887.1; -.
DR   EMBL; U10579; AAA19257.1; -.
DR   EMBL; U72350; AAB17353.1; -.
DR   EMBL; U72349; AAB17352.1; -.
DR   EMBL; U34963; AAA77686.1; -.
DR   EMBL; S76513; AAC60701.1; ALT_INIT.
DR   EMBL; S78284; AAC60702.1; -.
DR   PDB; 1AF3; 07-JUL-97.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
KW   3D-structure.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       86    100       BH3.
FT   DOMAIN      129    148       BH1.
FT   DOMAIN      180    195       BH2.
FT   TRANSMEM    210    226       POTENTIAL.
FT   VARSPLIC    126    188       MISSING (IN ISOFORM BCL-X(S)).
FT   VARSPLIC    189    233       DTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
FT                                FSRK -> VRTTPLVCPPLVCLSSVEIPNCPFWSPGMVVED
FT                                IDYSGDIPGLL (IN ISOFORM BCL-X(BETA)).
FT   CONFLICT      6      6       R -> Q (IN REF. 1).
FT   CONFLICT     12     12       F -> S (IN REF. 2).
FT   CONFLICT     64     64       A -> E (IN REF. 2).
FT   CONFLICT     81     81       I -> L (IN REF. 4).
FT   CONFLICT    119    119       A -> V (IN REF. 4).
FT   CONFLICT    143    144       FF -> SS (IN REF. 4).
FT   CONFLICT    199    199       A -> T (IN REF. 4).
FT   CONFLICT    201    201       A -> P (IN REF. 4).
SQ   SEQUENCE   233 AA;  26158 MW;  2B62B6C63864BC8F CRC64;


  Query Match             42.6%;  Score 428.5;  DB 1;  Length 233;
  Best Local Similarity   41.3%;  Pred. No. 2e-31;
  Matches   93;  Conservative   22;  Mismatches   57;  Indels   53;  Gaps    4;

Qy      11 RALVADFVGYKLRQKGY----------------------------------------V 28
           | || ||: ||| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
           ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
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Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy     141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           :|||  |  |||: |  |:|: :|    |      : | | ||:|
Db     185 NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT  9
BCL2_CHICK
ID   BCL2_CHICK     STANDARD;      PRT;   233 AA.
AC   Q00709;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Apoptosis regulator Bcl-2.
GN   BCL2 OR BCL-2.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92375724; PubMed=1508712;
RA   Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT   "Isolation and characterization of the chicken bcl-2 gene: expression
RT   in a variety of tissues including lymphoid and neuronal organs in
RT   adult and embryo.";
RL   Nucleic Acids Res. 20:4187-4192(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell lymphoma;
RX   MEDLINE=92379084; PubMed=1511008;
RA   Cazals-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;
RT   "Molecular cloning and DNA sequence analysis of cDNA encoding chicken
RT   homologue of the Bcl-2 oncoprotein.";
RL   Biochim. Biophys. Acta 1132:109-113(1992).
CC   -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC       including factor-dependent lymphohematopoietic and neural cells.
CC       Regulates cell death by controlling the mitochondrial membrane
CC       permeability. Appears to function in a feedback loop system with
CC       caspases. Inhibits caspase activity either by preventing the
CC       release of cytochrome c from the mitochondria and/or by binding to
CC       the apoptosis-activating factor (APAF-1).
CC   -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC       Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC       domains, and is necessary for anti-apoptotic activity (By
CC       similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC       membrane of the nuclear envelope and the endoplasmic reticulum.
CC   -!- TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen,
CC       kidney, heart, ovary and brain, with the highest levels in the
CC       thymus. In the embryo, highly levels expressed in all tissues with
CC       high levels in the bursa of Fabricius.
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC       for interaction with RAF-1 (By similarity).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; D11382; BAA01978.1; -.
DR   EMBL; D11381; BAA01978.1; JOINED.
DR   EMBL; Z11961; CAA78018.1; -.
DR   PIR; A37332; A37332.
DR   PIR; S24390; S24390.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Transmembrane; Mitochondrion.
FT   DOMAIN       10     30       BH4.
FT   DOMAIN       87    101       BH3.
FT   DOMAIN      130    149       BH1.
FT   DOMAIN      181    196       BH2.
FT   TRANSMEM    208    228       POTENTIAL.
FT   CONFLICT     64     64       E -> S (IN REF. 2).
FT   CONFLICT     67     82       GSAAASEVPPAEGLRP -> ARLLLVRCPRLRGCA
FT                                (IN REF. 2).
FT   CONFLICT    121    121       H -> T (IN REF. 2).
FT   CONFLICT    139    139       G -> V (IN REF. 2).
SQ   SEQUENCE   233 AA;  25687 MW;  5252555ACB6E4C3D CRC64;


  Query Match             42.1%;  Score 423.5;  DB 1;  Length 233;
  Best Local Similarity   38.0%;  Pred. No. 5.5e-31;
  Matches   87;  Conservative   32;  Mismatches   61;  Indels   49;  Gaps    4;

Qy       9 DTRALVADFVGYKLRQKGYVCGAG-------PGEGPAADP------------------- 41
           | | :|  :: ||| |:||   ||       |   ||| |
Db      10 DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPEPPGSA 69

Qy      42 ----------------LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSD 84
                           :| |:| |||||  |::| |: :: |||:|| :|  ||  | :
Db      70 AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE 129

Qy      85 ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGW 144
           |||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   | :||  :|||
Db     130 ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW 189

Qy     145 AEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
             |  |||:      | | : :| |::|:|:  | :|| :|:||:   |
Db     190 DAFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK 233


RESULT  10
BCL2_BOVIN
ID   BCL2_BOVIN     STANDARD;      PRT;   229 AA.
AC   O02718;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Apoptosis regulator Bcl-2.
GN   BCL2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HOLSTEIN; TISSUE=Thymus;
RA   Reyes R.A., Cockerell G.L.;
RT   "Bovine leukemia virus associated-leukemogenesis is correlated
```

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RT   with suppression of programmed cell death and increased expression
RT   of Bcl-2.";
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC       including factor-dependent lymphohematopoietic and neural cells.
CC       Regulates cell death by controlling the mitochondrial membrane
CC       permeability. Appears to function in a feedback loop system with
CC       caspases. Inhibits caspase activity either by preventing the
CC       release of cytochrome c from the mitochondria and/or by binding to
CC       the apoptosis-activating factor (APAF-1) (By similarity).
CC   -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC       Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC       domains, and is necessary for anti-apoptotic activity (By
CC       similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC       membrane of the nuclear envelope and the endoplasmic reticulum (By
CC       similarity).
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC       for interaction with RAF-1 (By similarity).
CC   -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC       anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC       on Ser-70 by PKC is required for the anti-apoptosis activity and
CC       occurs during the G2/M phase of the cell cycle(By similarity). In
CC       the absence of growth factors, Bcl2 appears to be phosphorylated
CC       by other protein kinases such as ERKs and stress-activated
CC       kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC       cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC       activity, causes the release of cytochrome c into the cytosol
CC       promoting further caspase activity (By similarity).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U92434; AAB53319.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
FT   DOMAIN       10     30       BH4.
FT   DOMAIN       64     68       POLY-PRO.
FT   DOMAIN       69     72       POLY-ALA.
FT   DOMAIN       83     97       BH3.
FT   DOMAIN      126    145       BH1.
FT   DOMAIN      177    192       BH2.
FT   TRANSMEM    202    223       POTENTIAL.
FT   SITE          34     35       CLEAVAGE (BY CASPASES) (BY SIMILARITY).
FT   MOD_RES       63     63       PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SQ   SEQUENCE   229 AA;  25099 MW;  AD1DD0AF98FFF11D CRC64;
```

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  Query Match             41.4%;  Score 416.5;  DB 1;  Length 229;
  Best Local Similarity   38.2%;  Pred. No. 2.3e-30;
  Matches   86;  Conservative   35;  Mismatches   59;  Indels   45;  Gaps    5;

Qy       9 DTRALVADFVGYKLRQKGYVCGAG------------------PGE------------- 35
           | | :|  :: ||| |:||   ||                   ||
Db      10 DNREIVMKYIHYKLSQRGYEWDAGDAGAAPPGAAPAPGILSSQPGRTPAPSRTSPPPPPA 69

Qy      36 ---GPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQ 88
             |||  |    :|  :| |||:|  |:|| |:::::|||:|| :|::||  | :|||:
Db      70 AAAGPAPSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARERFATVVEELFR 129

Qy      89 GGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFT 148
           | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||  :|||  |
Db     130 DGVNWGRIVAFFEFGGVMCVESVNREMSPLVDSIALWMTEYLNRHLHTWIQDNGGWDAFV 189

Qy     149 ALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
           |||       | | : :| |:: :|: |: :|| :|:||:   |
Db     190 ELYG----PSMRPLFDFSWLSLKALLSLAL-VGACITLGAYLGHK 229


RESULT  11
BCL2_RAT
ID   BCL2_RAT       STANDARD;      PRT;   236 AA.
AC   P49950; Q62837; Q64032;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Apoptosis regulator Bcl-2.
GN   BCL2 OR BCL-2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=94193015; PubMed=8144041;
RA   Sato T., Irie S., Krajewski S., Reed J.C.;
RT   "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
RL   Gene 140:291-292(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Ovary;
RX   MEDLINE=95129487; PubMed=7828536;
RA   Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
RT   "Expression of members of the bcl-2 gene family in the immature rat
RT   ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT   cell apoptosis is associated with decreased bax and constitutive
RT   bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
RL   Endocrinology 136:232-241(1995).
RN   [3]
RP   SEQUENCE OF 19-172 FROM N.A.
RX   MEDLINE=95059917; PubMed=7969891;
RA   Castren E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H.,
RA   Lindholm D.;
RT   "bcl-2 messenger RNA is localized in neurons of the developing and
RT   adult rat brain.";
RL   Neuroscience 61:165-177(1994).
CC   -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC       including factor-dependent lymphohematopoietic and neural cells.
CC       Regulates cell death by controlling the mitochondrial membrane
CC       permeability. Appears to function in a feedback loop system with
CC       caspases. Inhibits caspase activity either by preventing the
CC       release of cytochrome c from the mitochondria and/or by binding to
CC       the apoptosis-activating factor (APAF-1).
CC   -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC       Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC       domains, and is necessary for anti-apoptotic activity (By
CC       similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC       membrane of the nuclear envelope and the endoplasmic reticulum.
CC   -!- TISSUE SPECIFICITY: Expressed in a variety of tissues, with
```

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CC       highest levels in reproductive tissues. In the adult brain,
CC       expression is localized in mitral cells of the olfactory bulb,
CC       granule and pyramidal neurons of hippocampus, pontine nuclei,
CC       cerebellar granule neurons, and in ependymal cells. In prenatal
CC       brain, expression is higher and localized in the neuroepithelium
CC       and in the cortical plate.
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC       for interaction with RAF-1 (By similarity).
CC   -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC       anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC       on Ser-70 by PKC is required for the anti-apoptosis activity and
CC       occurs during the G2/M phase of the cell cycle. In the absence of
CC       growth factors, Bcl2 appears to be phosphorylated by other protein
CC       kinases such as ERKs and stress-activated kinases.
CC       Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC       cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC       activity, causes the release of cytochrome c into the cytosol
CC       promoting further caspase activity (By similarity).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L14680; AAA53662.1; -.
DR   EMBL; U34964; AAA77687.1; -.
DR   EMBL; S74122; -; NOT_ANNOTATED_CDS.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
FT   DOMAIN       10     30       BH4.
FT   DOMAIN       90    104       BH3.
FT   DOMAIN      133    152       BH1.
FT   DOMAIN      184    199       BH2.
FT   TRANSMEM    209    230       POTENTIAL.
FT   SITE          34     35       CLEAVAGE (BY CASPASES) (BY SIMILARITY).
FT   MOD_RES       70     70       PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
FT   CONFLICT      42     42       A -> R (IN REF. 2).
FT   CONFLICT     157    157       E -> G (IN REF. 1).
FT   CONFLICT     164    164       S -> Y (IN REF. 2).
FT   CONFLICT     212    212       L -> Q (IN REF. 2).
SQ   SEQUENCE   236 AA;  26622 MW;  E7688CB9071A872A CRC64;


  Query Match             41.1%;  Score 414;  DB 1;  Length 236;
  Best Local Similarity   36.2%;  Pred. No. 4e-30;
  Matches   84;  Conservative   34;  Mismatches   62;  Indels   52;  Gaps    3;

Qy       9 DTRALVADFVGYKLRQKGY---------------------------------------- 27
           | | :|  :: ||| |:||
Db      10 DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRAAPTPGIFSFQPESNRTPAVHRDTAART 69

Qy      28 ------VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                 |  |||   |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db      70 SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
           | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  || :
Db     130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy     142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
           |||  |  |||       | | : :| |::|:|: |: :|| :|:||:   |
Db     190 GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236


RESULT  12
BCL2_MOUSE
ID   BCL2_MOUSE     STANDARD;      PRT;   236 AA.
AC   P10417; P10418;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Apoptosis regulator Bcl-2.
GN   BCL2 OR BCL-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC   STRAIN=BALB/C; TISSUE=Liver;
RX   MEDLINE=87187643; PubMed=3032455;
RA   Negrini M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.;
RT   "Molecular analysis of mbcl-2: structure and expression of the murine
RT   gene homologous to the human gene involved in follicular lymphoma.";
RL   Cell 49:455-463(1987).
RN   [2]
RP   REVISIONS TO 221-222.
RX   MEDLINE=92375724; PubMed=1508712;
RA   Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT   "Isolation and characterization of the chicken bcl-2 gene: expression
RT   in a variety of tissues including lymphoid and neuronal organs in
RT   adult and embryo.";
RL   Nucleic Acids Res. 20:4187-4192(1992).
RN   [3]
RP   PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.
RX   MEDLINE=97277291; PubMed=9115213;
RA   Ito T., Deng X., Carr B., May W.S. Jr.;
RT   "Bcl-2 phosphorylation required for anti-apoptosis function.";
RL   J. Biol. Chem. 272:11671-11673(1997).
RN   [4]
RP   DEPHOSPHORYLATION BY PP2A.
RX   MEDLINE=99069407; PubMed=9852076;
RA   Deng X., Ito T., Carr B., Mumby M., May W.S. Jr.;
RT   "Reversible phosphorylation of Bcl2 following interleukin 3 or
RT   bryostatin 1 is mediated by direct interaction with protein
RT   phosphatase 2A*.";
RL   J. Biol. Chem. 273:34157-34163(1998).
CC   -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC       including factor-dependent lymphohematopoietic and neural cells.
CC       Regulates cell death by controlling the mitochondrial membrane
CC       permeability. Appears to function in a feedback loop system with
CC       caspases. Inhibits caspase activity either by preventing the
CC       release of cytochrome c from the mitochondria and/or by binding to
CC       the apoptosis-activating factor (APAF-1).
CC   -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC       Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC       domains, and is necessary for anti-apoptotic activity (By
CC       similarity). Also interacts with APAF-1 and RAF-1.
CC   -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC       membrane of the nuclear envelope and the endoplasmic reticulum.
CC   -!- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta;
CC       are produced by alternative splicing.
CC   -!- TISSUE SPECIFICITY: Expressed in a variety of tissues.
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
```

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CC       for interaction with RAF-1.
CC   -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC       anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC       on Ser-70 by PKC is required for the anti-apoptosis activity and
CC       occurs during the G2/M phase of the cell cycle. In the absence of
CC       growth factors, Bcl2 appears to be phosphorylated by other protein
CC       kinases such as ERKs and stress-activated kinases.
CC       Dephosphorylated by protein phosphatase 2A (PP2A).
CC   -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC       cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC       activity, causes the release of cytochrome c into the cytosol
CC       promoting further caspase activity.
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L31532; AAA37282.1; -.
DR   EMBL; M16506; AAA37282.1; JOINED.
DR   EMBL; M16506; AAA37281.1; -.
DR   PIR; A25960; TVMSA1.
DR   PIR; B25960; TVMSB1.
DR   PIR; E37332; E37332.
DR   HSSP; Q07817; 1MAZ.
DR   MGD; MGI:88138; Bcl2.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Alternative splicing; Transmembrane; Mitochondrion;
KW   Phosphorylation.
FT   DOMAIN       10     30       BH4.
FT   DOMAIN       90    104       BH3.
FT   DOMAIN      133    152       BH1.
FT   DOMAIN      184    199       BH2.
FT   TRANSMEM    209    230       POTENTIAL.
FT   SITE         34     35       CLEAVAGE (BY CASPASES) (BY SIMILARITY).
FT   MOD_RES      70     70       PHOSPHORYLATION (BY PKC).
FT   VARSPLIC    193    236       DAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYL
FT                                GHK -> VGACLVE (IN ISOFORM BETA).
SQ   SEQUENCE   236 AA;  26425 MW;  AA85EF6B0766BE0A CRC64;


  Query Match             41.0%;  Score 413;  DB 1;  Length 236;
  Best Local Similarity   37.5%;  Pred. No. 4.9e-30;
  Matches   87;  Conservative   34;  Mismatches   59;  Indels   52;  Gaps    5;

Qy       9 DTRALVADFVGYKLRQKGYVCGAG----------PG---------------------- 34
           | | :|  :: ||| |:||   ||            ||
Db      10 DNREIVMKYIHYKLSQRGYEWDAGDADAAPLGAAPTPGIFSFQPESNPMPAVHREMAART 69

Qy      35 ---------EGPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                    |||  |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db      70 SPLRPLVATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
           | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||  :
Db     130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy     142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
           |||  |  |||       | | : :| |::|:|: |: :|| :|:||:   |
Db     190 GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236


RESULT  13
BCL2_HUMAN
ID   BCL2_HUMAN     STANDARD;      PRT;   239 AA.
AC   P10415; P10416; Q16197; Q13842;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Apoptosis regulator Bcl-2.
GN   BCL2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RX   MEDLINE=86259760; PubMed=3523487;
RA   Tsujimoto Y., Croce C.M.;
RT   "Analysis of the structure, transcripts, and protein products of
RT   bcl-2, the gene involved in human follicular lymphoma.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
RN   [2]
RP   REVISIONS TO 96; 110 AND 237.
RX   MEDLINE=92375724; PubMed=1508712;
RA   Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT   "Isolation and characterization of the chicken bcl-2 gene: expression
RT   in a variety of tissues including lymphoid and neuronal organs in
RT   adult and embryo.";
RL   Nucleic Acids Res. 20:4187-4192(1992).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX   MEDLINE=87002488; PubMed=2875799;
RA   Cleary M.L., Smith S.D., Sklar J.;
RT   "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-
RT   2/immunoglobulin transcript resulting from the t(14;18)
RT   translocation.";
RL   Cell 47:19-28(1986).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX   MEDLINE=88196071; PubMed=2834197;
RA   Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S.,
RA   Goldman P., Korsmeyer S.J.;
RT   "Alternative promoters and exons, somatic mutation and deregulation
RT   of the Bcl-2-Ig fusion gene in lymphoma.";
RL   EMBO J. 7:123-131(1988).
RN   [5]
RP   SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS NHL.
RX   MEDLINE=92096610; PubMed=1339299;
RA   Tanaka S., Louie D.C., Kant J.A., Reed J.C.;
RT   "Frequent incidence of somatic mutations in translocated BCL2
RT   oncogenes of non-Hodgkin's lymphomas.";
RL   Blood 79:229-237(1992).
RN   [6]
RP   SUBCELLULAR LOCATION.
RX   MEDLINE=91066924; PubMed=2250705;
RA   Hockenbery D., Nunez G., Milliman C., Schreiber R.D., Korsmeyer S.J.;
RT   "Bcl-2 is an inner mitochondrial membrane protein that blocks
RT   programmed cell death.";
RL   Nature 348:334-336(1990).
RN   [7]
RP   MUTAGENESIS.
RX   MEDLINE=94239528; PubMed=8183370;
RA   Yin X.-M., Oltvai Z.N., Korsmeyer S.J.;
RT   "BH1 and BH2 domains of Bcl-2 are required for inhibition of
RT   apoptosis and heterodimerization with Bax.";
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RL   Nature 369:321-323(1994).
RN   [8]
RP   CLEAVAGE BY CASPASES, AND MUTAGENESIS.
RX   MEDLINE=98057466; PubMed=9395403;
RA   Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,
RA   Ueno K., Hardwick J.M.;
RT   "Conversion of Bcl-2 to a Bax-like death effector by caspases.";
RL   Science 278:1966-1988(1997).
RN   [9]
RP   REVIEW ON PHOSPHORYLATION.
RX   MEDLINE=21260650; PubMed=11368354;
RA   Ruvolo P.P., Deng X., May W.S.;
RT   "Phosphorylation of Bcl2 and regulation of apoptosis.";
RL   Leukemia 15:515-522(2001).
RN   [10]
RP   PHOSPHORYLATION BY ASK1/JNK1.
RX   MEDLINE=20036804; PubMed=10567572;
RA   Yamamoto K., Ichijo H., Korsmeyer S.J.;
RT   "BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal
RT   protein kinase pathway normally activated at G(2)/M.";
RL   Mol. Cell. Biol. 19:8469-8478(1999).
CC   -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC       including factor-dependent lymphohematopoietic and neural cells.
CC       Regulates cell death by controlling the mitochondrial membrane
CC       permeability. Appears to function in a feedback loop system with
CC       caspases. Inhibits caspase activity either by preventing the
CC       release of cytochrome c from the mitochondria and/or by binding to
CC       the apoptosis-activating factor (APAF-1).
CC   -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC       Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC       domains, and is necessary for anti-apoptotic activity (By
CC       similarity). Also interacts with APAF-1 and RAF-1.
CC   -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC       membrane of the nuclear envelope and the endoplasmic reticulum.
CC   -!- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta;
CC       are produced by alternative splicing.
CC   -!- TISSUE SPECIFICITY: Expressed in a variety of tissues.
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC       for interaction with RAF-1.
CC   -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC       anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC       on Ser-70 by PKC is required for the anti-apoptosis activity and
CC       occurs during the G2/M phase of the cell cycle. In the absence of
CC       growth factors, Bcl2 appears to be phosphorylated by other protein
CC       kinases such as ERKs and stress-activated kinases.
CC       Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC       cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC       activity, causes the release of cytochrome c into the cytosol
CC       promoting further caspase activity.
CC   -!- DISEASE: Involved in follicular lymphoma (FL) (also known as type
CC       II chronic lymphatic leukemia) by a chromosomal translocation
CC       t(14;18)(q32;q21) which involves Bcl2 and immunoglobulin gene
CC       regions.
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M13994; AAA51813.1; ALT_SEQ.
DR   EMBL; M13995; AAA51814.1; ALT_SEQ.
DR   EMBL; M14745; AAA35591.1; -.
DR   EMBL; X06487; CAA29778.1; -.
DR   EMBL; S72602; AAD14111.1; ALT_SEQ.
DR   PIR; A29409; TVHUA1.
DR   PIR; B29409; TVHUB1.
DR   PIR; A24428; TVHUBC.
DR   PIR; C37332; C37332.
DR   PIR; D37332; D37332.
DR   HSSP; Q07817; 1MAZ.
DR   MIM; 151430; -.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Proto-oncogene; Apoptosis; Alternative splicing; Transmembrane;
KW   Mitochondrion; Phosphorylation; Chromosomal translocation;
KW   Polymorphism; Disease mutation.
FT   DOMAIN       10     30       BH4.
FT   DOMAIN       93    107       BH3.
FT   DOMAIN      136    155       BH1.
FT   DOMAIN      187    202       BH2.
FT   TRANSMEM    212    233       POTENTIAL.
FT   SITE          34     35       CLEAVAGE (BY CASPASE-3).
FT   MOD_RES       70     70       PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
FT   VARSPLIC     196    239       DAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYL
FT                                 GHK -> VGASGDVS (IN ISOFORM BETA).
FT
FT   VARIANT       7      7       T -> S.
FT                                 /FTId=VAR_000827.
FT   VARIANT      59     59       P -> S (IN NON-HODGKINS-LYMPHOMA; SOMATIC
FT                                 MUTATION).
FT                                 /FTId=VAR_000828.
FT   VARIANT      93     93       V -> I (IN NON-HODGKINS-LYMPHOMA; SOMATIC
FT                                 MUTATION).
FT                                 /FTId=VAR_000829.
FT   MUTAGEN      34     34       D->A: ABOLISHES CLEAVAGE BY CASPASE-3.
FT   MUTAGEN      64     64       D->A: NO EFFECT ON CLEAVAGE BY CASPASE-3.
FT   MUTAGEN     145    145       G->A: NO HETERODIMERIZATION WITH BAX AND
FT                                 LOSS OF ANTI-APOPTOTIC ACTIVITY.
FT   MUTAGEN     188    188       W->A: NO HETERODIMERIZATION WITH BAX AND
FT                                 LOSS OF ANTI-APOPTOTIC ACTIVITY.
FT   CONFLICT     48     48       I -> F (IN REF. 4).
FT   CONFLICT     59     59       P -> T (IN REF. 3).
FT   CONFLICT    117    117       S -> R (IN REF. 3).
FT   CONFLICT    129    129       R -> C (IN REF. 4).
SQ   SEQUENCE   239 AA;  26266 MW;  3C49F2B714DC9CCB CRC64;


  Query Match             41.0%;  Score 412.5;  DB 1;  Length 239;
  Best Local Similarity   37.0%;  Pred. No. 5.5e-30;
  Matches   87;  Conservative   34;  Mismatches   59;  Indels   55;  Gaps    5;

Qy       9 DTRALVADFVGYKLRQKGYVCGAG------------------PGE---------- 35
           | | :|  :: ||| |:||   ||                    ||
Db      10 DNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAPAPGIFSSQPGHTPHPAASRDPVART 69

Qy      36 ------------GPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQR 78
                       |||  |    :|  :| |||:|  |:|| |:::::|||:|| :|: |
Db      70 SPLQTPAAPGAAAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGR 129

Qy      79 FTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWI 138
           |  | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||
Db     130 FATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWI 189

Qy     139 HSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
             :|||  |  |||       | | : :| |::|:|: |: :|| :|:||:   |
Db     190 QDNGGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 239
```

}

```
RESULT  14
BCL2_CRILO
ID   BCL2_CRILO     STANDARD;      PRT;   236 AA.
AC   Q9JJV8;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Apoptosis regulator Bcl-2.
GN   BCL2.
OS   Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Cricetulus.
OX   NCBI_TaxID=10030;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=20431763; PubMed=10973819;
RA   Tomicic M.T., Christmann M., Kaina B.;
RT   "Cloning and functional analysis of cDNA encoding the hamster Bcl-2
RT   protein.";
RL   Biochem. Biophys. Res. Commun. 275:899-903(2000).
RN   [2]
RP   SEQUENCE FROM N.A., AND CLEAVAGE BY CASPASES.
RX   MEDLINE=21092839; PubMed=11181062;
RA   Tomicic M.T., Kaina B.;
RT   "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9
RT   and caspase-3.";
RL   Biochem. Biophys. Res. Commun. 281:404-408(2001).
CC   -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC       including factor-dependent lymphohematopoietic and neural cells.
CC       Regulates cell death by controlling the mitochondrial membrane
CC       permeability. Appears to function in a feedback loop system with
CC       caspases. Inhibits caspase activity either by preventing the
CC       release of cytochrome c from the mitochondria and/or by binding to
CC       the apoptosis-activating factor (APAF-1) (By similarity).
CC   -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC       Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC       domains, and is necessary for anti-apoptotic activity (By
CC       similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC       membrane of the nuclear envelope and the endoplasmic reticulum.
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC       for interaction with RAF-1 (By similarity).
CC   -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC       anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC       on Ser-70 by PKC is required for the anti-apoptosis activity and
CC       occurs during the G2/M phase of the cell cycle (By similarity). In
CC       the absence of growth factors, Bcl2 appears to be phosphorylated
CC       by other protein kinases such as ERKs and stress-activated kinases
CC       (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A)
CC       (By similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC       cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC       activity, causes the release of cytochrome c into the cytosol
CC       promoting further caspase activity.
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AJ271720; CAB92245.1; -.
DR   HSSP; P53563; 1AF3.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
FT   DOMAIN       10     30       BH4.
FT   DOMAIN       90    104       BH3.
FT   DOMAIN      133    152       BH1.
FT   DOMAIN      184    199       BH2.
FT   TRANSMEM    209    230       POTENTIAL.
FT   SITE         64     65       CLEAVAGE (BY CASPASE-3 AND CASPASE-9).
FT   MOD_RES      70     70       PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SQ   SEQUENCE   236 AA;  26491 MW;  BECADF1EF3337228 CRC64;


  Query Match             40.0%;  Score 403;  DB 1;  Length 236;
  Best Local Similarity   35.3%;  Pred. No. 3.8e-29;
  Matches   82;  Conservative   34;  Mismatches   64;  Indels   52;  Gaps    3;

Qy       9 DTRALVADFVGYKLRQKGY---------------------------------------- 27
           | | :|  :: ||| |:||
Db      10 DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART 69

Qy      28 ------VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                 |   ||   |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db      70 SPLRPIVATTGPTLSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
           | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||  :
Db     130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy     142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
           |||  |  |||       | | : :| |::|:|: |: :|| :|:| :   |
Db     190 GGWDAFVELYG----PSVRPLFDFSWLSLKTLLSLAL-VGACITLGTYLGHK 236


RESULT  15
AR11_XENLA
ID   AR11_XENLA     STANDARD;      PRT;   204 AA.
AC   Q91828;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Apoptosis regulator R11 (XR11).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Head;
RX   MEDLINE=95331613; PubMed=7607538;
RA   Cruz-Reyes J., Tata J.R.;
RT   "Cloning, characterization and expression of two Xenopus bcl-2-like
RT   cell-survival genes.";
RL   Gene 158:171-179(1995).
CC   -!- FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC   -!- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
CC       BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND
CC       ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
```

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CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X82461; CAA57844.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
KW   Apoptosis; Transmembrane.
FT   DOMAIN      101    120       BH1.
FT   DOMAIN      152    167       BH2.
FT   TRANSMEM    181    198       POTENTIAL.
SQ   SEQUENCE   204 AA;  23379 MW;  3BFC6BE6DDA4CA03 CRC64;


  Query Match             36.8%;  Score 371;  DB 1;  Length 204;
  Best Local Similarity   42.1%;  Pred. No. 2.4e-26;
  Matches   82;  Conservative   25;  Mismatches   62;  Indels   26;  Gaps    4;

Qy      10 TRALVADFVGYKLRQKGYVC----------------------GAGPGEGPAADPLHQAMR 47
           :| ||  ||  || |    |                      | |  :|   : : ||:
Db       5 SRDLVEKFVSKKLSQ-NEACRKFSNNPNPMPYLMEPSTSERPGEGATQGIVEEEVLQALL 63

Qy      48 AAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALC 107
           | :||| |::| |||| :|||:|  :||| | ||  |||: | ||||:|||| || |||
Db      64 EATEEFELRYQRAFSDLTSQLHITQDTAQQSFQQVMGELFRDGTNWGRIVAFFSFGRALC 123

Qy     108 AESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLRE--G 165
           || |||| |: :: :||| |||  |  |:  :|||  |  |||  |  ::|  :|  |
Db     124 VESANKEMTDLLPRIVQWMVNYLEHTLQPWMQENGGWEAFVGLYGKNAAAQSRESQERFG 183

Qy     166 NWASVRTVLTGAVAL 180
             ::  :|||  ||
Db     184 RLLTI-VMLTGVFAL 197


Search completed: June 10, 2002, 10:32:13
Job time: 346 sec
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 10:24:47 ; Search time 46.07 Seconds
(without alignments)
724.724 Million cell updates/sec

Title: US-09-155-327E-7
Perfect score: 1007
Sequence: 1 MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	996	98.9	193	11	O88996	O88996 rattus norv
2	761	75.6	178	11	Q9CYW5	Q9cyw5 mus musculu
3	440.5	43.7	233	6	Q9MYW4	Q9myw4 oryctolagus
4	435.5	43.2	233	11	O35844	O35844 mus musculu
5	431.5	42.9	233	6	Q9N1A2	Q9n1a2 sus scrofa
6	428.5	42.6	233	6	Q9MZS7	Q9mzs7 ovis aries
7	403	40.0	238	13	Q90Z98	Q90z98 brachydanio
8	401	39.8	180	6	Q9BDD5	Q9bdd5 bos taurus
9	401	39.8	217	11	Q99N35	Q99n35 mus musculu
10	399	39.6	236	11	Q923R6	Q923r6 cricetulus
11	398.5	39.6	180	6	Q9BDX7	Q9bdx7 bos taurus
12	374.5	37.2	188	11	Q9QWX2	Q9qwx2 mus musculu
13	374.5	37.2	235	11	O35843	O35843 mus musculu
14	373.5	37.1	188	4	Q9H1R6	Q9h1r6 homo sapien
15	373	37.0	204	13	Q90ZH2	Q90zh2 xenopus lae
16	347	34.5	219	11	Q99N36	Q99n36 mus musculu
17	189	18.8	209	11	Q9JK59	Q9jk59 rattus norv
18	185	18.4	170	11	Q9WUI5	Q9wui5 rattus norv
19	176.5	17.5	192	13	Q9I9N4	Q9i9n4 brachydanio
20	171.5	17.0	221	13	Q98U13	Q98u13 xenopus lae
21	168.5	16.7	125	4	Q9H1R5	Q9h1r5 homo sapien
22	163	16.2	58	11	Q9R1B3	Q9r1b3 rattus norv
23	162	16.1	235	5	Q967D2	Q967d2 geodia cydo
24	159.5	15.8	163	6	Q9MZS6	Q9mzs6 ovis aries
25	153	15.2	173	11	Q9JKL3	Q9jk13 rattus norv
26	148.5	14.7	218	5	Q9N754	Q9n754 suberites d
27	146.5	14.5	179	4	Q9NYG7	Q9nyg7 homo sapien
28	144	14.3	149	6	Q9GMG7	Q9gmg7 ovis aries
29	143	14.2	177	13	Q90ZN1	Q90zn1 gallus gall
30	142.5	14.2	179	12	Q9E1F2	Q9elf2 meleagrid h
31	141	14.0	255	13	Q9I9N3	Q9i9n3 brachydanio
32	139	13.8	211	13	Q9W6F1	Q9w6f1 gallus gall
33	135	13.4	114	4	Q9NR76	Q9nr76 homo sapien
34	135	13.4	212	4	Q9UMX3	Q9umx3 homo sapien
35	131.5	13.1	213	11	O35425	O35425 rattus norv
36	131	13.0	162	12	Q9DH00	Q9dh00 meleagrid h
37	130.5	13.0	213	4	Q9UL32	Q9ul32 homo sapien
38	130.5	13.0	213	13	Q9I8I2	Q9i8i2 gallus gall
39	130.5	13.0	213	13	Q9DGJ5	Q9dgj5 gallus gall
40	125.5	12.5	330	11	Q9Z1P3	Q9z1p3 rattus norv
41	125	12.4	174	13	Q9W6F2	Q9w6f2 gallus gall
42	123.5	12.3	331	11	P97287	P97287 mus musculu
43	122.5	12.2	91	11	Q923W5	Q923w5 peromyscus
44	121.5	12.1	91	11	Q923W6	Q923w6 peromyscus
45	117	11.6	204	4	Q9HD36	Q9hd36 homo sapien

ALIGNMENTS

RESULT 1
O88996
ID O88996 PRELIMINARY; PRT; 193 AA.
AC O88996;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE BCL-W.
GN BCL-W.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE=99292146; PubMed=10366024;
RA Hamner S., Skoglosa Y., Lindholm D.;
RT "Differential expression of bcl-w and bcl-x messenger RNA in the
RT developing and adult rat nervous system.";
RL Neuroscience 91:673-684(1999).
DR EMBL; AF096291; AAC64200.1; -.
DR HSSP; Q07817; 1MAZ.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR000712; Bcl_2.
DR InterPro; IPR003093; BH4.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 193 AA; 20820 MW; 36D6742F4529AFB4 CRC64;

Query Match 98.9%; Score 996; DB 11; Length 193;

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  Best Local Similarity   98.4%;  Pred. No. 2.4e-80;
  Matches  190;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||:||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 GALVTVGAFFASK 193


RESULT   2
Q9CYW5
ID   Q9CYW5      PRELIMINARY;      PRT;   178 AA.
AC   Q9CYW5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BCL2-LIKE 2.
GN   BCL2L2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK013244; BAB28740.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   MGD; MGI:108052; Bcl212.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   InterPro; IPR003093; BH4.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   178 AA;  19147 MW;  E2D4C3F79528E9D7 CRC64;
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  Query Match           75.6%;  Score 761;  DB 11;  Length 178;
  Best Local Similarity   95.3%;  Pred. No. 1.2e-59;
  Matches  143;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy     121 QVQEWMVAYLETRLADWIHSSGGWAEFTAL 150
           |||:||||||||||||||||||||   : |
Db     121 QVQDWMVAYLETRLADWIHSSGGWVRSSQL 150


RESULT   3
Q9MYW4
ID   Q9MYW4      PRELIMINARY;      PRT;   233 AA.
AC   Q9MYW4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   BCL-X.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Knott J.C., Robertson L., James E.R.;
RT   "Rabbit Bcl-X.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY005131; AAF88137.1; -.
DR   HSSP; P53563; 1AF3.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   InterPro; IPR003093; BH4.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   233 AA;  25986 MW;  12F0F30344D53F93 CRC64;
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  Query Match           43.7%;  Score 440.5;  DB 6;  Length 233;
  Best Local Similarity   42.0%;  Pred. No. 3.5e-31;
  Matches   94;  Conservative   22;  Mismatches   57;  Indels   51;  Gaps    4;

Qy      11 RALVADFVGYKLRQKGYVC--------------GAG----------------PGEGPAA 39
           | || ||: ||| ||||                 | |                | : ||
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTGPEMETPSAINGNPAWHPADSPAV 65

Qy      40 D------------------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
           :                  : ||:| |||||| |:|| |||| :|||:|||:| | | |
Db      66 NGATGHSSSLDAREVIPMTAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 125

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
           | :|||: | ||||:|||| || ||| |||:|||| || ::  ||  ||   |  ||  :
Db     126 VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMEVLVSRIAAWMATYLNDHLEPWIQEN 185

Qy     142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           |||  |  |||: |  |:|: :|    |       : | | ||:|
Db     186 GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229
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RESULT   4
O35844
ID   O35844      PRELIMINARY;      PRT;   233 AA.
AC   O35844;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BCL-XL.
GN   BCL2L.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B6/CBA; TISSUE=THYMUS;
RX   MEDLINE=98051053; PubMed=9390687;
RA   Yang X.-F., Weber G.F., Cantor H.;
RT   "A novel Bcl-x isoform connected to the T cell receptor regulates
RT   apoptosis in T cells.";
RL   Immunity 7:629-639(1997).
DR   EMBL; U51278; AAC53459.1; -.
DR   HSSP; P53563; 1AF3.
DR   MGD; MGI:88139; Bcl2l.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   InterPro; IPR003093; BH4.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   233 AA;  26033 MW;  3083F2D8327E072E CRC64;


  Query Match             43.2%;  Score 435.5;  DB 11;  Length 233;
  Best Local Similarity   41.8%;  Pred. No. 9.6e-31;
  Matches   94;  Conservative   22;  Mismatches   56;  Indels   53;  Gaps    4;

Qy      11 RALVADFVGYKLRQKGY----------------------------------------V 28
           | || ||: ||| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy     141 SGGWAEFTALYGDGALEEARRLREG--NWASVRTVLTGAVALGAL 183
           :|||  |  |||: |  |:|: :||   |      : | | ||:|
Db     185 NGGWDTFVDLYGNNAAAESRKGKEGFNRWFLTGMTVAGVVLLGSL 229


RESULT   5
Q9N1A2
ID   Q9N1A2      PRELIMINARY;      PRT;   233 AA.
AC   Q9N1A2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANTI-APOPTOTIC REGULATOR BCL-XL.
GN   BCL-XL.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART;
RA   Lee T.L., Canty J.M.;
RT   "PCR Cloning of a Porcine bcl-xL cDNA from Heart.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF216205; AAF33212.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   InterPro; IPR003093; BH4.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   233 AA;  26047 MW;  2FA312818B25E17D CRC64;


  Query Match             42.9%;  Score 431.5;  DB 6;  Length 233;
  Best Local Similarity   41.8%;  Pred. No. 2.2e-30;
  Matches   94;  Conservative   21;  Mismatches   57;  Indels   53;  Gaps    4;

Qy      11 RALVADFVGYKLRQKGY----------------------------------------V 28
           | || ||: ||| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQE 184

Qy     141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           :|||  |  |||: |  |:|: :|   |      | | | ||:|
Db     185 NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTLAGVVLLGSL 229


RESULT   6
Q9MZS7
ID   Q9MZS7      PRELIMINARY;      PRT;   233 AA.
AC   Q9MZS7;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   BCL-X LONG PROTEIN.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=OVARY;
RA   Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;
RT   "Bcl-x in the sheep ovary.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF164517; AAF89532.1; -.
DR   HSSP; P53563; 1AF3.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   InterPro; IPR003093; BH4.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
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DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   233 AA;  26134 MW;  012BFA1382762915 CRC64;


  Query Match           42.6%;  Score 428.5;  DB 6;  Length 233;
  Best Local Similarity   40.6%;  Pred. No. 4e-30;
  Matches   91;  Conservative   23;  Mismatches   59;  Indels   51;  Gaps    4;

Qy      11 RALVADFVGYKLRQKGY--------------------------VCGAGP----GEGPAA 39
           | || ||: ||| ||||                          |     : ||
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESDMETPSAINGNPSWHLADSPAV 65

Qy      40 D------------------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
           :                  : ||:| |||||| |:|| |||| :|||:|||:| | | |
Db      66 NGATGHSRSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 125

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
           | :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||  :
Db     126 VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQEN 185

Qy     142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           |||  |  |||: |  |:|: :|    |      : | | ||:|
Db     186 GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT   7
Q90Z98
ID   Q90Z98      PRELIMINARY;      PRT;   238 AA.
AC   Q90Z98;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BCL-XL-LIKE PROTEIN 1.
GN   BLP1.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21299061; PubMed=11406282;
RA   Chen M.-C., Gong H.-Y., Cheng C., Wang J.-P., Hong J., Wu J.-L.;
RT   "Cloning and characterization of zfBLP1, a Bcl-XL homologue from the
RT   zebrafish, Danio rerio(1).";
RL   Biochim. Biophys. Acta 1519:127-133(2001).
DR   EMBL; AF317837; AAK81706.1; -.
SQ   SEQUENCE   238 AA;  26253 MW;  6E58394933EEFDDB CRC64;


  Query Match           40.0%;  Score 403;  DB 13;  Length 238;
  Best Local Similarity   36.6%;  Pred. No. 7.3e-28;
  Matches   87;  Conservative   27;  Mismatches   62;  Indels   62;  Gaps    6;

Qy      11 RALVADFVGYKLRQKGYVC------------------GAG-------------------- 32
           | ||  |: ||| |: | |                   | |
Db       6 RELVVFFIKYKLSQRNYPCNHIGLTEDTNRTDGAEENGEGAAGATTLVNGTMNRTNASST 65

Qy      33 --PGEGPAADPLHQ------------AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQR 78
             | : ||: |  |            |:| : :||| |: | |:||::|||:|| :| |
Db      66 GTPPQSPASSPQRQTNGSGGLDAVKEALRDSANEFELRYSRAFNDLSSQLHITPATAYQS 125

Qy      79 FTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWI 138
           |  | ||:|: | ||||:|  | || ||| | | ||| ||||:: |||  ||:  :  ||
Db     126 FESVMDEVFRDGVNWGRIVGLFAFGGALCVECVEKEMSPLVGRIAEWMTVYLDNHIQPWI 185

Qy     139 HSSGGWAEFTALYGDGALEEARRLREG--NWA-SVRTVLTGAVALGALVTVGAFFASK 193
           |  |||  |  ::|  |  |:|: :|    |  :  |:|||       | ||   | |
Db     186 QSQGGWERFAEIFGKDAAAESRKSQESFKKWLFAGMTLLTG-------VVVGGLIAQK 236


RESULT   8
Q9BDD5
ID   Q9BDD5      PRELIMINARY;      PRT;   180 AA.
AC   Q9BDD5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANTI-APOPTOTIC REGULATOR BCL-XL (FRAGMENT).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Amills M., Bouzat J.;
RT   "Characterization of the bovine bcl-xL gene and related pseudogenes.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF245488; AAK31307.1; -.
DR   EMBL; AF245489; AAK31308.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   SMART; SM00337; BCL; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
FT   NON_TER       1      1
FT   NON_TER     180    180
SQ   SEQUENCE   180 AA;  20062 MW;  95DC436F95DABDA6 CRC64;


  Query Match           39.8%;  Score 401;  DB 6;  Length 180;
  Best Local Similarity   53.5%;  Pred. No. 7.7e-28;
  Matches   76;  Conservative   19;  Mismatches   45;  Indels    2;  Gaps    1;

Qy      44 QAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFG 103
           ||:| |||||| |:|| |||| :|||:|||:| | | || :|||: | ||||:|||| ||
Db      38 QALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFG 97

Qy     104 AALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLR 163
            ||| |||:|||: || ::  ||  ||   |  ||  :|||  |  |||: |  |:|: :
Db      98 GALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQ 157

Qy     164 E--GNWASVRTVLTGAVALGAL 183
           |    |      : | | ||:|
Db     158 ERFNRWFLTGMTVAGVVLLGSL 179


RESULT   9
Q99N35
ID   Q99N35      PRELIMINARY;      PRT;   217 AA.
AC   Q99N35;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   B-CELL LEUKEMIA/LYMPHOMA X (FRAGMENT).
GN   BCLX.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SVJ;
RA   Yang X.-F., Cantor H.;
RT   "Novel cDNA structure and genomic organization of apoptosis regulatory
```

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RT   gene Bcl-x-gamma.";
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF133282; AAK15455.1; -.
DR   EMBL; AF133281; AAK15455.1; JOINED.
DR   HSSP; P53563; 1AF3.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   SMART; SM00337; BCL; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   217 AA;  24234 MW;  3B5A4E809A7DEF18 CRC64;


  Query Match             39.8%;  Score 401;  DB 11;  Length 217;
  Best Local Similarity   53.5%;  Pred. No. 9.7e-28;
  Matches   76;  Conservative   19;  Mismatches   45;  Indels    2;  Gaps    1;

Qy      44 QAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFG 103
           ||:| |||||| |:|| |||| :|||:|||:| | | || :|||: | ||||:|||| ||
Db      72 QALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFG 131

Qy     104 AALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLR 163
            ||| |||:|||: || ::  ||  ||   |  ||  :|||  |  |||: |  |:|: :
Db     132 GALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESRKGQ 191

Qy     164 E--GNWASVRTVLTGAVALGAL 183
           |    |      : | | ||:|
Db     192 ERFNRWFLTGMTVAGVVLLGSL 213


RESULT  10
Q923R6
ID   Q923R6      PRELIMINARY;      PRT;   236 AA.
AC   Q923R6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   B-CELL LYMPHOMA PROTEIN 2.
GN   BCL2.
OS   Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Cricetulus.
OX   NCBI_TaxID=10030;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lai D.Z., Chen W., Wang H.T.;
RT   "Construction of a robust CHO cell line for biopharmaceutical use.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF404339; AAK92201.1; -.
SQ   SEQUENCE   236 AA;  26500 MW;  BEDF052EF32CA8B8 CRC64;


  Query Match             39.6%;  Score 399;  DB 11;  Length 236;
  Best Local Similarity   35.3%;  Pred. No. 1.6e-27;
  Matches   82;  Conservative   32;  Mismatches   66;  Indels   52;  Gaps    3;

Qy       9 DTRALVADFVGYKLRQKGY---------------------------------------- 27
           | | :|  :: ||| |:||
Db      10 DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART 69

Qy      28 ------VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                 |   ||   |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db      70 SPLRPIVATTGPTLSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
           | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||  :
Db     130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy     142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
           |||  |  |||       | | : :| |: |:|  |: :|| :|:| :   |
Db     190 GGWDAFVELYG----PSVRPLFDFSWLSLXTLLNLAL-VGACITLGTYLGHK 236


RESULT  11
Q9BDX7
ID   Q9BDX7      PRELIMINARY;      PRT;   180 AA.
AC   Q9BDX7;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANTI-APOPTOTIC REGULATOR BCL-XL (FRAGMENT).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Amills M., Bouzat J.;
RT   "Characterization of the bovine bcl-xL gene and related pseudogenes.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF245487; AAK31306.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   SMART; SM00337; BCL; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
FT   NON_TER       1      1
FT   NON_TER     180    180
SQ   SEQUENCE   180 AA;  20056 MW;  62C4C0BD0555A9EF CRC64;


  Query Match             39.6%;  Score 398.5;  DB 6;  Length 180;
  Best Local Similarity   47.1%;  Pred. No. 1.3e-27;
  Matches   82;  Conservative   23;  Mismatches   58;  Indels   11;  Gaps    3;

Qy      20 YKLRQKGYVCGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVT 71
           : |      | || ||   ::|          : ||:| |||||| |:|| |||| :|||:|
Db       7 WHLEDSPAVNGA-PGHSRSSDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHIT 65

Qy      72 PGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLE 131
           ||:| | | || :|||: | ||||:|| | || ||| |||:|||: || ::  ||  ||
Db      66 PGTAYQSFEQVVNELFRDGVNWGRIVASFSFGGALCVESVDKEMQVLVSRIATWMATYLN 125

Qy     132 TRLADWIHSSGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
             |  ||  :|||  |  |||: |  |:|: :|    |      : | | ||:|
Db     126 DHLEPWIQENGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 179


RESULT  12
Q9QWX2
ID   Q9QWX2      PRELIMINARY;      PRT;   188 AA.
AC   Q9QWX2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BCL-X (FRAGMENT).
GN   BCL2L.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20350651; PubMed=10894153;
RA   Rucker E.B. III, Dierisseau P., Wagner K.U., Garrett L.,
RA   Wynshaw-Boris A., Flaws J.A., Hennighausen L.;
RT   "Bcl-x and Bax regulate mouse primordial germ cell survival and
```

```
RT   apoptosis during embryogenesis.";
RL   Mol. Endocrinol. 14:1038-1052(2000).
DR   EMBL; AF088904; AAC72232.1; -.
DR   HSSP; P53563; 1AF3.
DR   MGD; MGI:88139; Bcl2l.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   InterPro; IPR003093; BH4.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
FT   NON_TER     188    188
SQ   SEQUENCE   188 AA;  21126 MW;  4E62F8356D248E52 CRC64;


  Query Match             37.2%;  Score 374.5;  DB 11;  Length 188;
  Best Local Similarity   42.9%;  Pred. No. 1.8e-25;
  Matches   79;  Conservative   16;  Mismatches   38;  Indels   51;  Gaps    3;

Qy      11 RALVADFVGYKLRQKGY----------------------------------------V 28
           | || ||: ||| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy     141 SGGW 144
           :|||
Db     185 NGGW 188


RESULT  13
O35843
ID   O35843      PRELIMINARY;      PRT;   235 AA.
AC   O35843;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BCL-X-GAMMA.
GN   BCL2L.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B6/CBA; TISSUE=THYMUS;
RX   MEDLINE=98051053; PubMed=9390687;
RA   Yang X.-F., Weber G.F., Cantor H.;
RT   "A novel Bcl-x isoform connected to the T cell receptor regulates
RT   apoptosis in T cells.";
RL   Immunity 7:629-639(1997).
DR   EMBL; U51277; AAC53458.1; -.
DR   HSSP; P53563; 1AF3.
DR   MGD; MGI:88139; Bcl2l.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   InterPro; IPR003093; BH4.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   235 AA;  26122 MW;  649D914C2D5378F6 CRC64;


  Query Match             37.2%;  Score 374.5;  DB 11;  Length 235;
  Best Local Similarity   42.9%;  Pred. No. 2.4e-25;
  Matches   79;  Conservative   16;  Mismatches   38;  Indels   51;  Gaps    3;

Qy      11 RALVADFVGYKLRQKGY----------------------------------------V 28
           | || ||: ||| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy     141 SGGW 144
           :|||
Db     185 NGGW 188


RESULT  14
Q9H1R6
ID   Q9H1R6      PRELIMINARY;      PRT;   188 AA.
AC   Q9H1R6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BA243J16.1.1 (BCL2-LIKE 1 (ISOFORM 1)) (FRAGMENT).
GN   BCL2L1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Brown A.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL160175; CAC10003.1; -.
DR   HSSP; Q07817; 1LXL.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   InterPro; IPR003093; BH4.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
FT   NON_TER     188    188
SQ   SEQUENCE   188 AA;  21029 MW;  7074B6095145C324 CRC64;


  Query Match             37.1%;  Score 373.5;  DB 4;  Length 188;
  Best Local Similarity   42.9%;  Pred. No. 2.2e-25;
  Matches   79;  Conservative   16;  Mismatches   38;  Indels   51;  Gaps    3;

Qy      11 RALVADFVGYKLRQKGY----------------------------------------V 28
           | || ||: ||| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
```

```
Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE 184

Qy     141 SGGW 144
           :|||
Db     185 NGGW 188
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RESULT 15
Q90ZH2
ID Q90ZH2 PRELIMINARY; PRT; 204 AA.
AC Q90ZH2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE BCL-XL.
GN BCL-XL.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakajima K., Yaoita Y.;
RT "Muscle cell death occurs in the regressing tail of tadpole by a
RT suicide mechanism.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB055494; BAB62748.1; -.
SQ SEQUENCE 204 AA; 23189 MW; 1BEF1B904E29D84A CRC64;

Query Match 37.0%; Score 373; DB 13; Length 204;
Best Local Similarity 42.8%; Pred. No. 2.7e-25;
Matches 83; Conservative 24; Mismatches 63; Indels 24; Gaps 4;

```
Qy      10 TRALVADFVGYKLRQ----------------KGYVCGAGPGEGP----AADPLHQAMRA 48
           :| ||  ||  || |                |      ||||       : : ||:
Db       5 SRDLVEKFVSKKLSQNEACRKFSNNPQPNAISNGTSTSERPGEGATQGIVEEEVLQALLE 64

Qy      49 AGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCA 108
           | :||| |::| |||| :|||:|  :||| | ||  |||: | ||||:|||| || |||
Db      65 ATEEFELRYQRAFSDLTSQLHITQDTAQQSFQQVMGELFRDGTNWGRIVAFFSFGRALCV 124

Qy     109 ESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLRE--GN 166
           || ||||  |: :: :||| |||  |  |:  :|||  |  |||  |  ::|  :|  |
Db     125 ESANKEMTDLLPRIVQWMVNYLEHTLQPWMQENGGWEAFVGLYGKNAAAQSRESQERFGR 184

Qy     167 WASVRTVLTGAVAL 180
             .   ::  :|||  ||
Db     185 LLTI-VMLTGVFAL 197
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Search completed: June 10, 2002, 10:31:19
Job time: 392 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 10:25:47 ; Search time 55.16 Seconds
(without alignments)
388.637 Million cell updates/sec

Title: US-09-155-327E-9
Perfect score: 1009
Sequence: 1 MATPASTPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1006	99.7	193	20	AAY05531	Mouse Bcl-w protei
2	1002	99.3	193	19	AAW61391	Rat bcl-y protein.
3	1002	99.3	193	20	AAW97391	The rat bcl-y prot
4	997	98.8	192	20	AAW97393	Protein sequence o
5	997	98.8	193	20	AAY05530	Human Bcl-w protei
6	992	98.3	193	19	AAW61392	Human bcl-y protei
7	992	98.3	193	20	AAW97392	The human bcl-y pr
8	990	98.1	193	18	AAW36047	Human bcl-w protei
9	990	98.1	193	20	AAY05532	Human Bcl-w protei
10	987	97.8	192	20	AAW97394	Mammalian bcl-y pr
11	970.5	96.2	192	20	AAY05533	Mouse Bcl-w protei
12	879	87.1	168	18	AAW36048	Mouse bcl-w protei
13	756	74.9	365	19	AAW59884	Amino acid sequenc
14	429.5	42.6	411	22	AAU00219	Bcl-X1-DTR apoptos
15	425.5	42.2	233	22	AAB73303	Rat wild-type Bcl-
16	424.5	42.1	233	16	AAR68887	Human thymus BCL-X
17	424.5	42.1	233	17	AAW05821	Bcl-XL protein. H
18	424.5	42.1	233	18	AAW31530	Human anti-apoptot
19	424.5	42.1	233	21	AAY83223	Bcl-x polypeptide.
20	424.5	42.1	233	21	AAY69969	Human Bcl-XL prote
21	424.5	42.1	233	22	AAG64262	Human Bcl-XL prote
22	424.5	42.1	233	22	AAB50538	Human Bcl-xL prote
23	424.5	42.1	233	22	AAB47515	Protein encoded by
24	422	41.8	225	18	AAW19396	"Deprenyl" (RTM)-i
25	421.5	41.8	233	22	AAB73304	Mutant rat Bcl-xL
26	412.5	40.9	239	22	AAG64037	Human Bcl-2 protei
27	409	40.5	236	22	AAB35131	Murine Bcl-2. Mus
28	408.5	40.5	239	20	AAW87810	A human Bcl-2 prot
29	408.5	40.5	239	22	AAB74127	Human bcl-2. Homo
30	408.5	40.5	239	22	AAB35130	Human Bcl-2. Homo
31	406.5	40.3	239	9	AAP80987	Sequence of bcl-2-
32	406.5	40.3	239	14	AAR42312	Bcl-2 oncogene pro
33	406.5	40.3	239	16	AAR70331	Human bcl-2 protei
34	406.5	40.3	239	16	AAR71404	Human bcl-2 alpha
35	406.5	40.3	239	19	AAW40217	Human bcl-2. Homo
36	406.5	40.3	239	20	AAW87812	A human Bcl-2-alph
37	406.5	40.3	239	22	AAE08573	Human Bcl-2 protei
38	406.5	40.3	239	22	AAG64035	Human Bcl-2 protei
39	406.5	40.3	239	22	AAG64036	Human Bcl-2 protei
40	406.5	40.3	239	22	AAB74129	Human bcl-2alpha.
41	406.5	40.3	239	22	AAB48288	Human BCL-2 protei
42	406.5	40.3	239	22	AAB50537	Human Bcl-2 protei
43	406.5	40.3	272	19	AAY21120	Human bcl2 proto-o
44	406.5	40.3	485	22	AAU00222	LFn-Bcl-XL apoptos
45	404	40.0	232	17	AAW01019	Apoptosis-blocking

ALIGNMENTS

RESULT 1
AAY05531
ID AAY05531 standard; Protein; 193 AA.
XX
AC AAY05531;
XX
DT 05-JUL-1999 (first entry)
XX
DE Mouse Bcl-w protein essential for spermatogenesis.
XX
KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
KW animal model.
XX
OS Mus sp.
XX
PN WO9913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU00764.
XX
PR 16-SEP-1997; 97AU-0009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
XX
DR WPI; 1999-243890/20.
DR N-PSDB; AAX25133.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w
XX
PS Claim 2; Page 35; 52pp; English.

```
XX
CC   The present sequence is mouse Bcl-w, a pro-survival member of the
CC   Bcl-2 family which is widely expressed and which is essential for
CC   spermatogenesis. The invention relates generally to a method of
CC   treatment and to an animal model for the identification of
CC   molecules and genetic sequences useful for inducing or reducing
CC   fertility of male animals. Methods are provided for the treatment
CC   of infertility, or for reducing fertility, by modulating
CC   spermatogenesis. An animal model carries a mutation is at least
CC   one allele of the human or murine bcl-w gene (see AAX25132-35) or in
CC   a gene associated with bcl-w. Such animals have disorganised
CC   seminferous tubules and are substantially infertile, but possess no
CC   other major abnormalities as determined by histological examination.
CC   They can be used to screen for therapeutic molecules including
CC   genetic sequences capable of inducing, enhancing or otherwise
CC   facilitating spermatogenesis in animals, or which can induce
CC   infertility.
XX
SQ   Sequence   193 AA;


  Query Match             99.7%;  Score 1006;  DB 20;  Length 193;
  Best Local Similarity   99.5%;  Pred. No. 5.5e-102;
  Matches  192;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db       1 matpastpdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 fsdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvg 120

Qy     121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 qvqdwmvayletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgaval 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 galvtvgaffask 193


RESULT   2
AAW61391
ID   AAW61391 standard; Protein; 193 AA.
XX
AC   AAW61391;
XX
DT   02-OCT-1998  (first entry)
XX
DE   Rat bcl-y protein.
XX
KW   bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
OS   Rattus sp.
XX
PN   US5789201-A.
XX
PD   04-AUG-1998.
XX
PF   11-FEB-1997;   97US-0798897.
XX
PR   23-FEB-1996;   96US-0012201.
PR   11-FEB-1997;   97US-0798897.
XX
PA   (COCE-) COCENSYS INC.
XX
PI   Guastella J;
XX
DR   WPI; 1998-446079/38.
DR   N-PSDB; V283333.
XX
PT   Nucleic acids encoding B-cell lymphoma-y protein - useful for
PT   producing recombinant protein for use in treating uncontrolled cell
PT   growth e.g. cancers
XX
PS   Example; Fig 3A; 27pp; English.
XX
CC   The mammalian bcl-y protein is a member of the bcl-2 family, components
CC   in the cell death pathway. The bcl-2 family have both apoptotic activity
CC   and the apoptosis blocking activity. bcl-y falls in the apoptosis
CC   activity category. The recombinant protein may be used to prevent
CC   uncontrolled cell growth, either by its direct administration to
CC   recombinant genetic constructs to increase its expression in vivo. Also,
CC   antisense constructs can be used in disorders where prevention of cell
CC   death is desired.
XX
SQ   Sequence   193 AA;


  Query Match             99.3%;  Score 1002;  DB 19;  Length 193;
  Best Local Similarity   99.0%;  Pred. No. 1.5e-101;
  Matches  191;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db       1 matpastpdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 fsdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvg 120

Qy     121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 qvqdwmvtyletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgaval 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 galvtvgaffask 193


RESULT   3
AAW97391
ID   AAW97391 standard; Protein; 193 AA.
XX
AC   AAW97391;
XX
DT   20-MAY-1999  (first entry)
XX
DE   The rat bcl-y protein.
XX
KW   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW   multiple sclerosis; myocardial infarction; vitally induced cell death;
KW   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW   premature cell death; cell death stimulator; prolonged cell life span;
KW   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW   parasite.
XX
OS   Rattus sp.
XX
PN   US5883229-A.
XX
PD   16-MAR-1999.
XX
PF   25-NOV-1997;   97US-0978523.
XX
PR   23-FEB-1996;   96US-0012201.
PR   11-FEB-1997;   97US-0798897.
PR   25-NOV-1997;   97US-0978523.
XX
PA   (COCE-) COCENSYS INC.
XX
PI   Guastella J;
XX
```

DR WPI; 1999-214150/18.
DR N-PSDB; AAX15945.
XX
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
PT for modulating programmed cell death
XX
PS Disclosure; Columns 15-18; 26pp; English.
XX
CC The present sequence represents rat bcl-y protein (Rbcl-y). The
CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and
CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral
CC sclerosis- conditions where cells under go premature cell death as a
CC result of triggers which may or may not be apparent. They may also be
CC used in this way to develop cell lines which remain viable in culture for
CC an extended period. In contrast, if they act as cell death stimulators,
CC Rbcl-y and Hbcl-y may be used to treat conditions associated with
CC prolonged cell life span such as cancer (especially kaposi's sarcoma and
CC lung cancer) and auto/hyperimmune diseases. They may also be used to
CC cause cell death in, and hence control, parasites.
XX
SQ Sequence 193 AA;

Query Match 99.3%; Score 1002; DB 20; Length 193;
Best Local Similarity 99.0%; Pred. No. 1.5e-101;
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db       1 matpastpdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 fsdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvg 120

Qy     121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 qvqdwmvtyletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgaval 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 galvtvgaffask 193
```

RESULT 4
AAW97393
ID AAW97393 standard; Protein; 192 AA.
XX
AC AAW97393;
XX
DT 20-MAY-1999 (first entry)
XX
DE Protein sequence of the specification.
XX
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW multiple sclerosis; myocardial infarction; vitally induced cell death;
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW premature cell death; cell death stimulator; prolonged cell life span;
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW parasite.
XX
OS Unidentified.
XX
PN US5883229-A.
XX
PD 16-MAR-1999.
XX
PF 25-NOV-1997; 97US-0978523.
XX
PR 23-FEB-1996; 96US-0012201.
PR 11-FEB-1997; 97US-0798897.
PR 25-NOV-1997; 97US-0978523.
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1999-214150/18.
XX
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
PT for modulating programmed cell death
XX
PS Disclosure; Columns 19-20; 26pp; English.
XX
CC The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
CC thought to be involved in programmed cell death (apoptosis and necrosis).
CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
CC with a disruption of the cell death pathway. If they act as cell death
CC inhibitors, they may be used in therapies to treat subjects suffering
CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular
CC degenerative diseases (especially multiple sclerosis), myocardial
CC infarction, vitally induced cell death, aging, spinal cord injuries and
CC amyotrophic lateral sclerosis- conditions where cells under go premature
CC cell death as a result of triggers which may or may not be apparent.
CC They may also be used in this way to develop cell lines which remain
CC viable in culture for an extended period. In contrast, if they act as
CC cell death stimulators, Rbcl-y and Hbcl-y may be used to treat
CC conditions associated with prolonged cell life span such as cancer
CC (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune
CC diseases. They may also be used to cause cell death in, and hence
CC control, parasites.
XX
SQ Sequence 192 AA;

Query Match 98.8%; Score 997; DB 20; Length 192;
Best Local Similarity 99.0%; Pred. No. 5.3e-101;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy       2 ATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
           |||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db       1 atpastpdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrtf 60

Qy      62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvgq 120

Qy     122 VQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
           |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 vqdwmvtyletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgavalg 180

Qy     182 ALVTVGAFFASK 193
           ||||||||||||
Db     181 alvtvgaffask 192
```

RESULT 5
AAY05530
ID AAY05530 standard; Protein; 193 AA.
XX
AC AAY05530;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human Bcl-w protein essential for spermatogenesis.
XX

```
KW   Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
KW   animal model.
XX
OS   Homo sapiens.
XX
PN   WO9913710-A1.
XX
PD   25-MAR-1999.
XX
PF   16-SEP-1998;   98WO-AU00764.
XX
PR   16-SEP-1997;   97AU-0009228.
XX
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI   Adams J, Cory S, Gibson L, Koentgen F, Print C;
XX
DR   WPI; 1999-243890/20.
DR   N-PSDB; AAX25132.
XX
PT   An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT   protein associated with Bcl-w
XX
PS   Claim 2; Page 33; 52pp; English.
XX
CC   The present sequence is human Bcl-w, a pro-survival member of the
CC   Bcl-2 family which is widely expressed and which is essential for
CC   spermatogenesis. The invention relates generally to a method of
CC   treatment and to an animal model for the identification of
CC   molecules and genetic sequences useful for inducing or reducing
CC   fertility of male animals. Methods are provided for the treatment
CC   of infertility, or for reducing fertility, by modulating
CC   spermatogenesis. An animal model carries a mutation is at least
CC   one allele of the human or murine bcl-w gene (see AAX25132-35) or in
CC   a gene associated with bcl-w. Such animals have disorganised
CC   seminferous tubules and are substantially infertile, but possess no
CC   other major abnormalities as determined by histological examination.
CC   They can be used to screen for therapeutic molecules including
CC   genetic sequences capable of inducing, enhancing or otherwise
CC   facilitating spermatogenesis in animals, or which can induce
CC   infertility.
XX
SQ   Sequence   193 AA;
```

```
  Query Match             98.8%;  Score 997;  DB 20;  Length 193;
  Best Local Similarity   98.4%;  Pred. No. 5.3e-101;
  Matches  190;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |||||| |||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db       1 matpasapdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 fsdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvg 120

Qy     121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 qvqewmvayletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgaval 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 galvtvgaffask 193
```

```
RESULT   6
AAW61392
ID   AAW61392 standard; Protein; 193 AA.
XX
AC   AAW61392;
XX
DT   02-OCT-1998  (first entry)
XX
DE   Human bcl-y protein.
XX
KW   bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
XX
OS   Homo sapiens.
XX
PN   US5789201-A.
XX
PD   04-AUG-1998.
XX
PF   11-FEB-1997;   97US-0798897.
XX
PR   23-FEB-1996;   96US-0012201.
PR   11-FEB-1997;   97US-0798897.
XX
PA   (COCE-) COCENSYS INC.
XX
PI   Guastella J;
XX
DR   WPI; 1998-446079/38.
DR   N-PSDB; AAV28334.
XX
PT   Nucleic acids encoding B-cell lymphoma-y protein - useful for
PT   producing recombinant protein for use in treating uncontrolled cell
PT   growth e.g. cancers
XX
PS   Example; Column 17/18; 27pp; English.
XX
CC   The mammalian bcl-y protein is a member of the bcl-2 family, components
CC   in the cell death pathway. The bcl-2 family have both apoptotic activity
CC   and the apoptosis blocking activity. bcl-y falls in the apoptosis
CC   activity category. The recombinant protein may be used to prevent
CC   uncontrolled cell growth, either by its direct administration to
CC   recombinant genetic constructs to increase its expression in vivo. Also,
CC   antisense constructs can be used in disorders where prevention of cell
CC   death is desired.
XX
SQ   Sequence   193 AA;
```

```
  Query Match             98.3%;  Score 992;  DB 19;  Length 193;
  Best Local Similarity   97.9%;  Pred. No. 1.9e-100;
  Matches  189;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |||||| |||||||| |||||:|||||||||||||||||||||||||||||||||||||||
Db       1 matpasapdtralvedfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 fsdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvg 120

Qy     121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 qvqewmvayletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgaval 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 galvtvgaffask 193
```

```
RESULT   7
AAW97392
ID   AAW97392 standard; Protein; 193 AA.
XX
AC   AAW97392;
XX
DT   20-MAY-1999  (first entry)
XX
DE   The human bcl-y protein.
XX
KW   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
```

```
KW   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW   multiple sclerosis; myocardial infarction; vitally induced cell death;
KW   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW   premature cell death; cell death stimulator; prolonged cell life span;
KW   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW   parasite.
XX
OS   Homo sapiens.
XX
PN   US5883229-A.
XX
PD   16-MAR-1999.
XX
PF   25-NOV-1997;   97US-0978523.
XX
PR   23-FEB-1996;   96US-0012201.
PR   11-FEB-1997;   97US-0798897.
PR   25-NOV-1997;   97US-0978523.
XX
PA   (COCE-) COCENSYS INC.
XX
PI   Guastella J;
XX
DR   WPI; 1999-214150/18.
DR   N-PSDB; AAX15946.
XX
PT   Novel bcl-y homologues of the rat and human bcl-2 protein  - useful
PT   for modulating programmed cell death
XX
PS   Claim 1; Columns 17-18; 26pp; English.
XX
CC   The present sequence represents human bcl-y protein (Hbcl-y). The
CC   specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and
CC   Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC   programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC   proteins may be used to treat conditions associated with a disruption of
CC   the cell death pathway. If they act as cell death inhibitors, they may be
CC   used in therapies to treat subjects suffering from: strokes, head trauma,
CC   Alzheimer's Disease, neural and muscular degenerative diseases
CC   (especially multiple sclerosis), myocardial infarction, vitally induced
CC   cell death, aging, spinal cord injuries and amyotrophic lateral
CC   sclerosis- conditions where cells under go premature cell death as a
CC   result of triggers which may or may not be apparent. They may also be
CC   used in this way to develop cell lines which remain viable in culture for
CC   an extended period. In contrast, if they act as cell death stimulators,
CC   Rbcl-y and Hbcl-y may be used to treat conditions associated with
CC   prolonged cell life span such as cancer (especially kaposi's sarcoma and
CC   lung cancer) and auto/hyperimmune diseases. They may also be used to
CC   cause cell death in, and hence control, parasites.
XX
SQ   Sequence   193 AA;
```

```
  Query Match             98.3%;  Score 992;  DB 20;  Length 193;
  Best Local Similarity   97.9%;  Pred. No. 1.9e-100;
  Matches  189;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |||||| ||||||| |||||:|||||||||||||||||||||||||||||||||||||||
Db       1 matpasapdtralvedfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 fsdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvg 120

Qy     121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 qvqewmvayletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgaval 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 galvtvgaffask 193
```

```
RESULT   8
AAW36047
ID   AAW36047 standard; Protein; 193 AA.
XX
AC   AAW36047;
XX
DT   22-APR-1998  (first entry)
XX
DE   Human bcl-w protein.
XX
KW   Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW   diagnosis; degenerative disease.
XX
OS   Homo sapiens.
XX
PN   WO9735971-A1.
XX
PD   02-OCT-1997.
XX
PF   27-MAR-1997;   97WO-AU00199.
XX
PR   27-MAR-1996;   96AU-0008965.
XX
PA   (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI   Adams JM,  Cory S,  Gibson LM,  Holmgreen SP;
XX
DR   WPI; 1997-489635/45.
DR   N-PSDB; AAT96577.
XX
PT   Nucleic acid encoding apoptosis related gene bcl-w - used to induce
PT   or inhibit cell survival, e.g. for treatment of cancer and
PT   degenerative diseases
XX
PS   Claim 6; Page 48; 86pp; English.
XX
CC   This sequence represents a novel human protein, bcl-w, encoded by the
CC   bcl-2 gene family and extracted from an adult brain library. This gene
CC   promotes cell survival, so its modulation is useful in treatment of
CC   cancer or auto-immune diseases, degenerative diseases (e.g. stroke,
CC   Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,
CC   ischaemia, human immunodeficiency virus infection or in cell transplants.
CC   Up-regulation of the gene can also be used to modify cell lines cultured
CC   in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
CC   and to increase survival of primary explants during genetic modification.
CC   It can be used to produce recombinant Bcl-w for therapy, diagnosis,
CC   antibody production or screening of potential modulators.
XX
SQ   Sequence   193 AA;
```

```
  Query Match             98.1%;  Score 990;  DB 18;  Length 193;
  Best Local Similarity   97.4%;  Pred. No. 3.1e-100;
  Matches  188;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |||||| ||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db       1 matpasapdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db      61 fsdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvafflfgaalcaesvnkemeplvg 120

Qy     121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 qvqewmvayletrlvdwihssggwaeftalygdgaleearrlregnwasvrtvltgaval 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 galvtvgaffask 193
```

```
RESULT   9
AAY05532
ID   AAY05532 standard; Protein; 193 AA.
XX
AC   AAY05532;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Human Bcl-w protein essential for spermatogenesis.
XX
KW   Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
KW   animal model.
XX
OS   Homo sapiens.
XX
PN   WO9913710-A1.
XX
PD   25-MAR-1999.
XX
PF   16-SEP-1998;   98WO-AU00764.
XX
PR   16-SEP-1997;   97AU-0009228.
XX
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI   Adams J,  Cory S,  Gibson L,  Koentgen F,  Print C;
XX
DR   WPI; 1999-243890/20.
DR   N-PSDB; AAX25134.
XX
PT   An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT   protein associated with Bcl-w
XX
PS   Disclosure; Page 37; 52pp; English.
XX
CC   The present sequence is described of a derivative of human Bcl-w
CC   (see also AAY05530), a pro-survival member of the Bcl-2 family that
CC   is widely expressed and which is essential for spermatogenesis.
CC   The invention relates generally to a method of treatment and to an
CC   animal model for the identification of molecules and genetic
CC   sequences useful for inducing or reducing fertility of male animals.
CC   Methods are provided for the treatment of infertility, or for
CC   reducing fertility, by modulating spermatogenesis.  An animal model
CC   carries a mutation is at least one allele of the human or murine
CC   bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w.
CC   Such animals have disorganised seminferous tubules and are
CC   substantially infertile, but possess no other major abnormalities
CC   as determined by histological examination.  They can be used to
CC   screen for therapeutic molecules including genetic sequences
CC   capable of inducing, enhancing or otherwise facilitating
CC   spermatogenesis in animals, or which can induce infertility.
XX
SQ   Sequence   193 AA;

  Query Match           98.1%;  Score 990;  DB 20;  Length 193;
  Best Local Similarity  97.4%;  Pred. No. 3.1e-100;
  Matches  188;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           ||||||  |||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db       1 matpasapdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db      61 fsdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvafflfgaalcaesvnkemeplvg 120

Qy     121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db     121 qvqewmvayletrlvdwihssggwaeftalygdgaleearrlregnwasvrtvltgaval 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 galvtvgaffask 193


RESULT  10
AAW97394
ID   AAW97394 standard; Protein; 192 AA.
XX
AC   AAW97394;
XX
DT   20-MAY-1999  (first entry)
XX
DE   Mammalian bcl-y protein.
XX
KW   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
KW   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;
KW   head trauma; Alzheimer's Disease; neural; muscular degenerative disease;
KW   multiple sclerosis; myocardial infarction; vitally induced cell death;
KW   aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;
KW   premature cell death; cell death stimulator; prolonged cell life span;
KW   Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
KW   parasite.
XX
OS   Mammalia.
XX
PN   US5883229-A.
XX
PD   16-MAR-1999.
XX
PF   25-NOV-1997;   97US-0978523.
XX
PR   23-FEB-1996;   96US-0012201.
PR   11-FEB-1997;   97US-0798897.
PR   25-NOV-1997;   97US-0978523.
XX
PA   (COCE-) COCENSYS INC.
XX
PI   Guastella J;
XX
DR   WPI; 1999-214150/18.
XX
PT   Novel bcl-y homologues of the rat and human bcl-2 protein  - useful
PT   for modulating programmed cell death
XX
PS   Claim 2; Columns 19-22; 26pp; English.
XX
CC   The present sequence represents a mammalian bcy-1 protein.
CC   The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y
CC   protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein
CC   thought to be involved in programmed cell death (apoptosis and necrosis).
CC   Rbcl-y and Hbcl-y proteins may be used to treat conditions associated
CC   with a disruption of the cell death pathway. If they act as cell death
CC   inhibitors, they may be used in therapies to treat subjects suffering
CC   from: strokes, head trauma, Alzheimer's Disease, neural and muscular
CC   degenerative diseases (especially multiple sclerosis), myocardial
CC   infarction, vitally induced cell death, aging, spinal cord injuries and
CC   amyotrophic lateral sclerosis- conditions where cells under go premature
CC   cell death as a result of triggers which may or may not be apparent.
CC   They may also be used in this way to develop cell lines which remain
CC   viable in culture for an extended period. In contrast, if they act as
CC   cell death stimulators, Rbcl-y and Hbcl-y may be used to treat
CC   conditions associated with prolonged cell life span such as cancer
CC   (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune
CC   diseases. They may also be used to cause cell death in, and hence
CC   control, parasites.
XX
SQ   Sequence   192 AA;

  Query Match           97.8%;  Score 987;  DB 20;  Length 192;
  Best Local Similarity  97.9%;  Pred. No. 6.6e-100;
  Matches  188;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy       2 ATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
           ||||| ||||||| |||||:|||||||||||||||||||||||||||||||||||||||||
Db       1 atpasapdtralvedfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrtf 60

Qy      62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvgq 120

Qy     122 VQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALG 181
           ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 vqewmvayletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgavalg 180

Qy     182 ALVTVGAFFASK 193
           ||||||||||||
Db     181 alvtvgaffask 192
```

RESULT 11
AAY05533
ID AAY05533 standard; Protein; 192 AA.
XX
AC AAY05533;
XX
DT 05-JUL-1999 (first entry)
XX
DE Mouse Bcl-w protein deritvative.
XX
KW Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
KW animal model.
XX
OS Mus sp.
XX
PN WO9913710-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-AU00764.
XX
PR 16-SEP-1997; 97AU-0009228.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Adams J, Cory S, Gibson L, Koentgen F, Print C;
XX
DR WPI; 1999-243890/20.
DR N-PSDB; AAX25135.
XX
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or
PT protein associated with Bcl-w
XX
PS Disclosure; Page 39; 52pp; English.
XX
CC The present sequence is described of a derivative of mouse Bcl-w
CC (see also AAY05531), a pro-survival member of the Bcl-2 family that
CC is widely expressed and which is essential for spermatogenesis.
CC The derivative lacks the 24 N-terminal amino acids of Bcl-w.
CC The invention relates generally to a method of treatment and to an
CC animal model for the identification of molecules and genetic
CC sequences useful for inducing or reducing fertility of male animals.
CC Methods are provided for the treatment of infertility, or for
CC reducing fertility, by modulating spermatogenesis. An animal model
CC carries a mutation is at least one allele of the human or murine
CC bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w.
CC Such animals have disorganised seminferous tubules and are
CC substantially infertile, but possess no other major abnormalities
CC as determined by histological examination. They can be used to
CC screen for therapeutic molecules including genetic sequences
CC capable of inducing, enhancing or otherwise facilitating
CC spermatogenesis in animals, or which can induce infertility.
XX
SQ Sequence 192 AA;

Query Match 96.2%; Score 970.5; DB 20; Length 192;
Best Local Similarity 96.4%; Pred. No. 4.2e-98;
Matches 186; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

```
Qy       1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mptpastpdtralvadfvgyrlrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 fsdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvg 120

Qy     121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||||:|||||||||||||||||:||||||||||:|||||||||| | ||:||||||
Db     121 qvqdwivayletrladwihssggwadftalygdgaledarrlregnwa-vstvvtgaval 179

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     180 galvtvgaffask 192
```

RESULT 12
AAW36048
ID AAW36048 standard; Protein; 168 AA.
XX
AC AAW36048;
XX
DT 22-APR-1998 (first entry)
XX
DE Mouse bcl-w protein.
XX
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW diagnosis; degenerative disease.
XX
OS Mus sp.
XX
PN WO9735971-A1.
XX
PD 02-OCT-1997.
XX
PF 27-MAR-1997; 97WO-AU00199.
XX
PR 27-MAR-1996; 96AU-0008965.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Adams JM, Cory S, Gibson LM, Holmgreen SP;
XX
DR WPI; 1997-489635/45.
DR N-PSDB; AAT96578.
XX
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce
PT or inhibit cell survival, e.g. for treatment of cancer and
PT degenerative diseases
XX
PS Claim 6; Page 50-51; 86pp; English.
XX
CC This sequence represents a novel protein, bcl-w, encoded by the mouse
CC bcl-2 gene family. This gene promotes cell survival, so its modulation
CC is useful in treatment of cancer or auto-immune diseases, degenerative
CC diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular
CC degeneration, hypoxia, ischaemia, human immunodeficiency virus infection
CC or in cell transplants. Up-regulation of the gene can also be used to
CC modify cell lines cultured in vivo, e.g. to develop new lines, to
CC facilitate isolation of hybridomas and to increase survival of primary
CC explants during genetic modification. It can be used to produce
CC recombinant Bcl-w for therapy, diagnosis, antibody production or
CC screening of potential modulators.
XX
SQ Sequence 168 AA;

Query Match 87.1%; Score 879; DB 18; Length 168;

```
  Best Local Similarity   97.6%;  Pred. No. 3.7e-88;
  Matches  164;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mptpastpdtralvadfvgyrlrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 fsdlaaqlhvtpgsaqqrftqvsdelfqgggpnwgrlvaffvfgaalcaesvnkemeplvg 120

Qy     121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWA 168
           |||||:||||||||||||||||:||||||||||:||||||||||
Db     121 qvqdwivayletrladwihssggwadftalygdgaledarrlregnwa 168


RESULT  13
AAW59884
ID   AAW59884 standard; Protein; 365 AA.
XX
AC   AAW59884;
XX
DT   20-NOV-1998  (first entry)
XX
DE   Amino acid sequence of the cDNA clone Bcl-like (HAICH29).
XX
KW   Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
KW   immunological disorder; autoimmune disease; anti-infectious agent.
XX
OS   Homo sapiens.
XX
PN   WO9831800-A2.
XX
PD   23-JUL-1998.
XX
PF   21-JAN-1998;   98WO-US00960.
XX
PR   21-JAN-1997;   97US-0034205.
PR   21-JAN-1997;   97US-0034204.
XX
PA   (AUCK-) AUCKLAND UNISERVICES LTD.
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Feng P,  Gentz RL,  Krissansen GW,  Ni J,  Rosen CA;
PI   Su JY;
XX
DR   WPI; 1998-414099/35.
DR   N-PSDB; AAV41925.
XX
PT   New isolated polynucleotides and encoded polypeptides - used to
PT   develop products for treating e.g. inflammatory diseases,
PT   infections, immunological disorders, autoimmune diseases, allergies
PT   or tumours
XX
PS   Claim 1; Fig 12A-12D; 120pp; English.
XX
CC   This is the amino acid sequence of the cDNA clone Bcl-like (HAICH29),
CC   used in the method of the invention.  The products of the clone can be
CC   used for treating conditions associated with abnormal expression of
CC   the polypeptides.  They can be used for e.g. treating chronic
CC   inflammatory diseases, immunological disorders, autoimmune diseases,
CC   inflammatory diseases, various allergies, and as anti-infectious agents.
CC   The products can also be used for detection and diagnosis.
XX
SQ   Sequence   365 AA;


  Query Match             74.9%;  Score 756;  DB 19;  Length 365;
  Best Local Similarity   97.9%;  Pred. No. 3.2e-74;
  Matches  141;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |||||| |||||||||||||:||||||||||||||||||||||||||||||||||||||||

Db       1 matpasapdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 fsdlaaqlhvtpgsaqqrftqvsdelfqgggpnwgrlvaffvfgaalcaesvnkemeplvg 120

Qy     121 QVQDWMVAYLETRLADWIHSSGGW 144
           |||:|||||||||||||||||||
Db     121 qvqewmvayletrladwihssggw 144


RESULT  14
AAU00219
ID   AAU00219 standard; Protein; 411 AA.
XX
AC   AAU00219;
XX
DT   31-MAY-2001  (first entry)
XX
DE   Bcl-Xl-DTR apoptosis-modifying fusion protein.
XX
KW   Human; Bcl-Xl-DTR; apoptosis; cancer; spinal muscular atrophy;
KW   diphtheria toxin receptor binding domain; DTR; neoplasm; tumour;
KW   hyper-proliferation; Alzheimer's disease; neurodegenerative disorder;
KW   transient ischaemic neuronal injury; stroke; spinal cord injury;
KW   Huntington's disease.
XX
OS   Chimeric - Homo sapiens.
OS   Chimeric - Corynebacterium diptheriae.
OS   Chimeric - Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          3..12
FT                   /note= "10x histidine tag"
FT   Domain          21..253
FT                   /note= "Bcl-Xl amino acids 1 to 233"
FT   Region          254..259
FT                   /note= "Linker amino acids, linking Bcl-Xl to diphtheria
FT                        toxin receptor binding domain (DTR)"
FT   Domain          260..411
FT                   /note= "DTR, diphtheria toxin receptor binding domain"
XX
PN   WO200112661-A2.
XX
PD   22-FEB-2001.
XX
PF   15-AUG-2000; 2000WO-US22293.
XX
PR   16-AUG-1999;   99US-0149220.
XX
PA   (HARD ) HARVARD COLLEGE.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Youle RJ,  Liu X,  Collier RJ;
XX
DR   WPI; 2001-218343/22.
DR   N-PSDB; AAS00247.
XX
PT   Novel fusion protein for modifying apoptosis in target cell and
PT   reducing apoptosis after transient ischaemic neuronal injury, has two
PT   domains which targets protein to a cell and modifies apoptotic response
PT   of cell  -
XX
PS   Claim 4; Page 56-57; 65pp; English.
XX
CC   The sequence represents the amino acid sequence of Bcl-Xl-DTR apoptosis-
CC   modifying fusion protein comprising Bcl-Xl sequence fused via a short
CC   linker to diphtheria toxin receptor binding domain (DTR). The functional
CC   apoptosis-modifying fusion protein is capable of binding a target cell
CC   and integrating into or crossing a cellular membrane of the target cell.
CC   comprising at least two domains, one of which targets the fusion protein
CC   to the target cell and another of which modifies an apoptotic response of
CC   the target cell. The fusion protein is useful for modifying (inhibiting
```

CC or enhancing) apoptosis in a target cell, such as neuron, lymphocyte,
CC cancer, neoplasm, macrophage, epithelial, stem, tumour or hyper-
CC proliferative cell or an adipocyte. It is also useful for reducing
CC apoptosis in a subject after transient ischaemic neuronal injury,
CC especially spinal cord injury. The fusion protein may be used to treat
CC various diseases and injury conditions through inhibition or enhancement
CC of apoptotic cellular response, including neurodegenerative disorders
CC such as Alzheimer's disease, Huntington's disease, spinal muscular
CC atrophy, stroke episodes and unregulated cell growth as in tumours and
CC various cancers. The apoptosis-modifying fusion protein can be delivered
CC effectively throughout the body and targeted to selective tissue and
CC cells.
XX
SQ Sequence 411 AA;

Query Match 42.6%; Score 429.5; DB 22; Length 411;
Best Local Similarity 39.5%; Pred. No. 2.1e-38;
Matches 92; Conservative 27; Mismatches 63; Indels 51; Gaps 4;

```
Qy      11 RALVADFVGYRLRQKGY----------------------------VCGAGP----GEGPAA 39
           | || ||: |:| ||||                             |     : ||
Db      26 relvvdflsyklsqkgyswsqfsdveenrteapegtesemetpsaingnpswhladspav 85

Qy      40 D------------------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
           :                  : ||:| |||||| |:|| |||| :|||:|||:| | | |
Db      86 ngatahsssldarevipmaavkqalreagdefelryrrafsdltsqlhitpgtayqsfeq 145

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
           | :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||  :
Db     146 vvnelfrdgvnwgrivaffsfggalcvesvdkemqvlvsriaawmatylndhlepwiqen 205

Qy     142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGALVTVGAFFAS 192
           |||  |  |||: |  |:|: :|    |      : | | ||:| :  |: |:
Db     206 ggwdtfvelygnnaaaesrkgqerfnrwfltgmtvagvvllgslfsrkaysaa 258
```

RESULT 15
AAB73303
ID AAB73303 standard; Protein; 233 AA.
XX
AC AAB73303;
XX
DT 22-MAY-2001 (first entry)
XX
DE Rat wild-type Bcl-xL protein.
XX
KW Rat Bcl-xL; apoptosis inhibitor; programmed cell death inhibitor;
KW wild-type; antiapoptotic; cell death-associated disease;
KW tissue transplant preservative.
XX
OS Rattus norvegicus.
XX
PN WO200112807-A1.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-JP05502.
XX
PR 17-AUG-1999; 99JP-0230642.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Ohta S, Asoh S;
XX
DR WPI; 2001-211219/21.
DR N-PSDB; AAF75960.
XX
PT Modified cDNA of rat bcl-x gene and encoded protein with membrane
PT permeability to enhance uptake for effective inhibition of cell death
PT e.g. apoptosis, useful in remedies for diseases associated with cell
PT death -
XX
PS Claim 6; Page 45-46; 56pp; Japanese.
XX
CC The invention relates to a mutant rat Bcl-x protein and the cDNA
CC encoding it. The mutant rat Bcl-x protein (Bcl-xFNK) has the
CC substitutions Y22F, Q26N, and R165K relative to the wild-type Bcl-xL
CC protein. The invention also encompasses recombinant vectors and host
CC cells comprising the modified nucleic acid sequence. The mutant Bcl-x
CC protein is able to permeate the cell membrane, thus enhancing its
CC ability to be taken up into a cell and to act as an inhibitor of
CC apoptosis (programmed cell death). Bcl-xFNK and nucleic acids encoding
CC it are useful in remedies for diseases associated with cell death and
CC in additives for maintaining the stability of transplanted cells and
CC organs. The present sequence represents wild-type rat Bcl-xL.
XX
SQ Sequence 233 AA;

Query Match 42.2%; Score 425.5; DB 22; Length 233;
Best Local Similarity 40.9%; Pred. No. 2.7e-38;
Matches 92; Conservative 23; Mismatches 57; Indels 53; Gaps 4;

```
Qy      11 RALVADFVGYRLRQKGY-------------------------------------------V 28
           | || ||: |:| ||||                                           |
Db       6 relvvdflsyklsqkgyswsqfsdveenrteapeeteperetpsaingnpswhladspav 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 nga-tghsssldarevipmaavkqalreagdefelryrrafsdltsqlhitpgtayqsfe 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 qvvnelfrdgvnwgrivaffsfggalcvesvdkemqvlvsriaswmatylndhlepwiqe 184

Qy     141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           :|||  |  |||: |  |:|: :|    |      : | | ||:|
Db     185 nggwdtfvdlygnnaaaesrkgqerfnrwfltgmtvagvvllgsl 229
```

Search completed: June 10, 2002, 10:25:48
Job time: 161 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 10:26:22 ; Search time 28.15 Seconds
(without alignments)
658.801 Million cell updates/sec

Title: US-09-155-327E-9
Perfect score: 1009
Sequence: 1 MATPASTPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	425.5	42.2	233	2	I49056	bcl-x long - mouse
2	424.5	42.1	233	2	B47537	apoptosis regulato
3	421.5	41.8	233	2	S51761	BCL-X protein - ra
4	420.5	41.7	233	2	A37332	transforming prote
5	411	40.7	232	2	S24390	transforming prote
6	408.5	40.5	239	1	TVHUA1	transforming prote
7	408	40.4	236	2	I67432	BCL-2 - rat (fragm
8	403	39.9	236	2	I53744	gene bcl-2 protein
9	402	39.8	236	1	TVMSA1	transforming prote
10	401.5	39.8	233	2	I67431	BCL-X-Long - rat
11	399	39.5	236	2	JC7383	B-cell lymphoma 2
12	375	37.2	190	2	A47537	apoptosis regulato
13	374.5	37.1	214	2	I49057	bcl-x transmembran
14	371.5	36.8	227	2	JE0203	apoptosis regulato
15	353	35.0	216	2	B37332	transforming prote
16	345.5	34.2	199	1	TVMSB1	transforming prote
17	342	33.9	205	1	TVHUB1	transforming prote
18	277.5	27.5	154	2	I58194	gene bcl-2 protein
19	179	17.7	170	2	I49055	bcl-x short - mous
20	174	17.2	211	2	S58873	Bak protein - huma
21	171	16.9	176	2	I67435	gene bcl-xshort pr
22	169	16.7	211	2	S58875	cdn-2 protein - hu
23	158.5	15.7	192	2	D47538	bcl-2-associated p
24	154	15.3	192	2	A47538	bcl-2-associated p
25	154	15.3	261	2	H88578	protein ced-9 [imp
26	154	15.3	280	2	A53189	apoptosis suppress
27	150.5	14.9	133	2	I53295	bcl-2-associated p
28	147.5	14.6	179	2	JC7255	Bax-delta protein
29	147.5	14.6	218	2	B47538	bcl-2-associated p
30	144	14.3	177	2	S54778	NR-13 protein - qu
31	141	14.0	255	2	JC7567	Mcl-1a protein - z
32	138.5	13.7	143	2	I38921	bcl-2-associated p
33	119	11.8	175	2	I39055	Bcl-2 related - hu
34	116	11.5	350	2	A47476	BCL2 homolog MCL1
35	105	10.4	172	2	I49449	hemopoietic-specif
36	88	8.7	185	2	B83217	hypothetical prote
37	86.5	8.6	301	2	T36534	probable lipase/es
38	86.5	8.6	3433	1	GNWVKV	genome polyprotein
39	86	8.5	270	2	AI2598	dihydrodipicolinat
40	86	8.5	279	2	B97381	dihydrodipicolinat
41	83.5	8.3	358	1	AJLCQB	glutamate--ammonia
42	83.5	8.3	872	2	H95160	alanyl-tRNA synthe
43	83.5	8.3	872	2	G98026	alanine--tRNA liga
44	82.5	8.2	3430	1	GNWVWV	genome polyprotein
45	81.5	8.1	886	2	A32758	beta-amyloid-like

ALIGNMENTS

RESULT 1
I49056
bcl-x long - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C;Accession: I49056; S52866
R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes
A;Reference number: I49055; MUID:95052604
A;Accession: I49056
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-233 <RES>
A;Cross-references: EMBL:U10101; NID:g506647; PIDN:AAA82173.1; PID:g506648
R;Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.
submitted to the EMBL Data Library, November 1994
A;Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line th
A;Reference number: S52866
A;Accession: S52866
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-233 <KAM>
A;Cross-references: EMBL:X83574; NID:g695622; PIDN:CAA58557.1; PID:g695623
C;Superfamily: bcl transforming protein

Query Match 42.2%; Score 425.5; DB 2; Length 233;
Best Local Similarity 40.9%; Pred. No. 4.3e-32;
Matches 92; Conservative 23; Mismatches 57; Indels 53; Gaps 4;

```
Qy      11 RALVADFVGYRLRQKGY----------------------------------------V 28
           | || ||: |:| ||||                                         |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy     141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           :||| |  |||: |  |:|: :|    |       : | | ||:|
Db     185 NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229
```

RESULT 2
B47537
apoptosis regulator bcl-xL - human
N;Alternate names: bcl-2-related protein

```
N;Contains: apoptosis regulator bcl-xS
C;Species: Homo sapiens (man)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C;Accession: B47537; C47537
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74, 597-608, 1993
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A;Reference number: A47537; MUID:93364977
A;Accession: B47537
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-233 <BOI>
A;Cross-references: GB:L20121; NID:g510900; PIDN:CAA80661.1; PID:g510901
A;Accession: C47537
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-69,'G',71-125,189-233 <BO2>
A;Cross-references: GB:L20122; NID:g623236; PIDN:CAA80662.1; PID:g623237
C;Genetics:
A;Gene: GDB:BCL2L
A;Cross-references: GDB:228079
C;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; apoptosis
F;1-233/Product: apoptosis regulator bcl-xL #status predicted <MAT>
F;1-125,189-233/Product: apoptosis regulator bcl-xS #status predicted <MA2>


  Query Match             42.1%;  Score 424.5;  DB 2;  Length 233;
  Best Local Similarity   40.2%;  Pred. No. 5.3e-32;
  Matches   90;  Conservative   24;  Mismatches   59;  Indels   51;  Gaps    4;

Qy      11 RALVADFVGYRLRQKGY--------------------------VCGAGP----GEGPAA 39
           | || ||: |:| ||||                          |     : ||
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65

Qy      40 D------------------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
           :                  : ||:| |||||| |:|| |||| :|||:|||:| | | |
Db      66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 125

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
           | :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||  :
Db     126 VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQEN 185

Qy     142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           |||  |  |||: |  |:|: :|    |      : | | ||:|
Db     186 GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT   3
S51761
BCL-X protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 02-Mar-2001
C;Accession: S51761; S51762
R;Michaelidis, T.M.
submitted to the EMBL Data Library, November 1994
A;Reference number: S51761
A;Accession: S51761
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <MIC>
A;Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57886.1; PID:g607177
A;Experimental source: embryonic; brain
A;Accession: S51762
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125,189-233 <MI2>
A;Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57887.1; PID:g607178
A;Experimental source: embryonic; brain
A;Note: smaller form due to splicing
C;Genetics:
A;Introns: 125/3
C;Superfamily: bcl transforming protein


  Query Match             41.8%;  Score 421.5;  DB 2;  Length 233;
  Best Local Similarity   40.8%;  Pred. No. 1e-31;
  Matches   91;  Conservative   23;  Mismatches   56;  Indels   53;  Gaps    4;

Qy      13 LVADFVGYRLRQKGY-------------------------------------------VCG 30
           || ||: |:| ||||                                           | |
Db       8 LVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAVNG 67

Qy      31 AGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQV 82
           |  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | | ||
Db      68 A-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQV 126

Qy      83 SDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSG 142
            :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||  :|
Db     127 VNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENG 186

Qy     143 GWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           ||  |  |||: |  |:|: :|    |      : | | ||:|
Db     187 GWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT   4
A37332
transforming protein (bcl-2-alpha) - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 23-Feb-1997
C;Accession: A37332; S35453
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a va
A;Reference number: A37332; MUID:92375724
A;Accession: A37332
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-233 <EGU>
A;Cross-references: EMBL:D11381
C;Genetics:
A;Introns: 189/3
C;Superfamily: bcl transforming protein
C;Keywords: mitochondrion; transforming protein; transmembrane protein


  Query Match             41.7%;  Score 420.5;  DB 2;  Length 233;
  Best Local Similarity   37.6%;  Pred. No. 1.3e-31;
  Matches   86;  Conservative   33;  Mismatches   61;  Indels   49;  Gaps    4;

Qy       9 DTRALVADFVGYRLRQKGYVCGAG-------PGEGPAADP------------------- 41
           | | :|  :: |:| |:||   ||       |   ||| |
Db      10 DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPEPPGSA 69

Qy      42 ----------------LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSD 84
                           :| |:| |||||  |::| |: :: |||:|| :|  ||  | :
Db      70 AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE 129

Qy      85 ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGW 144
           |||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   | :||  :|||
Db     130 ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW 189

Qy     145 AEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
             |  |||:      | | : :| |::|:|:  | :|| :|:|||:   |
Db     190 DAFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK 233


RESULT   5
S24390
transforming protein (Bcl-2) homolog - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S24390
R;Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.
Biochim. Biophys. Acta 1132, 109-113, 1992
```

A;Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue
A;Reference number: S24390; MUID:92379084
A;Accession: S24390
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-232 <CAZ>
A;Cross-references: EMBL:Z11961; NID:g62969; PIDN:CAA78018.1; PID:g62970
C;Superfamily: bcl transforming protein
C;Keywords: mitochondrion; transmembrane protein

Query Match 40.7%; Score 411; DB 2; Length 232;
Best Local Similarity 37.3%; Pred. No. 9.5e-31;
Matches 85; Conservative 33; Mismatches 62; Indels 48; Gaps 4;

```
Qy       9 DTRALVADFVGYRLRQKGYVCGAG-------PGEGPAADP---------------------- 41
           | | :|  :: |:| |:||   ||       |   |||.|
Db      10 DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPSPPARL 69

Qy      42 ----------------LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
                           :| |:| |||||  |::| |: :: |||:|| :|  ||  | :|
Db      70 LLVRCPRLRGCAAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTATGRFVAVVEE 129

Qy      86 LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWA 145
           ||: | || |:|||| ||  :| ||||:|| |||  :  ||  ||   | :||  :|||
Db     130 LFRDGVNWVRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGWD 189

Qy     146 EFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
            |  |||:      | | : :| |::|:|:  | :|| :|:||:   |
Db     190 AFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK 232
```

RESULT 6
TVHUA1
transforming protein bcl-2, splice form alpha - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change 15-Oct-1999
C;Accession: C37332; A29409; S02452; A24428; A27622; B27622
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
A;Reference number: A37332; MUID:92375724
A;Accession: C37332
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-239 <EGU>
A;Note: this report is a correction
R;Tsujimoto, Y.; Croce, C.M.
Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986
A;Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene
A;Reference number: A29409; MUID:86259760
A;Accession: A29409
A;Molecule type: mRNA
A;Residues: 1-95,'A',97-109,'G',111-236,'S',238-239 <TSU>
A;Cross-references: GB:M13994; NID:g179366; PIDN:AAA51813.1; PID:g179367
A;Note: this sequence has been corrected in reference A37332
R;Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeye
EMBO J. 7, 123-131, 1988
A;Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2
A;Reference number: S02452; MUID:88196071
A;Accession: S02452
A;Molecule type: mRNA
A;Residues: 1-239 <SET>
R;Cleary, M.L.; Smith, S.D.; Sklar, J.
Cell 47, 19-28, 1986
A;Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglo
A;Reference number: A24428; MUID:87002488
A;Accession: A24428
A;Molecule type: mRNA
A;Residues: 1-58,'T',60-116,'R',118-239 <CLE>
A;Cross-references: GB:M14745; NID:g179370; PIDN:AAA35591.1; PID:g179371
R;Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakhshi, A.
Oncogene Res. 2, 263-275, 1988

A;Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphom
A;Reference number: A27622; MUID:88217344
A;Accession: A27622
A;Molecule type: mRNA
A;Residues: 1-58,'T',60-239 <HUA>
A;Accession: B27622
A;Molecule type: DNA
A;Residues: 1-6,'S',8-58,'T',60-128,'C',130-239 <HUA2>
A;Note: the sequence was determined from the germline gene
C;Comment: Constitutive expression of BCL2 following t(14:18) chromosomal translocati
C;Genetics:
A;Gene: GDB:BCL2
A;Cross-references: GDB:119031; OMIM:151430
A;Map position: 18q21.3-18q21.3
C;Function:
A;Description: blocks apoptosis in hematopoietic cells
C;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; pr

Query Match 40.5%; Score 408.5; DB 1; Length 239;
Best Local Similarity 36.6%; Pred. No. 1.7e-30;
Matches 86; Conservative 35; Mismatches 59; Indels 55; Gaps 5;

```
Qy       9 DTRALVADFVGYRLRQKGYVCGAG-------------------PGE-------------- 35
           | | :|  :: |:| |:||   ||                    ||
Db      10 DNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAPAPGIFSSQPGHTPHPAASRDPVART 69

Qy      36 -------------GPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQR 78
                        |||  |    :|  :| |||:|  |:|| |:::::|||:|| :|: |
Db      70 SPLQTPAAPGAAAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGR 129

Qy      79 FTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWI 138
           |  | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   | ||
Db     130 FATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWI 189

Qy     139 HSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
             :|||  |  |||       | | : :| |::|:|: |: :|| :|:||:   |
Db     190 QDNGGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 239
```

RESULT 7
I67432
BCL-2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: I67432
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: eq
onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
A;Reference number: I53295; MUID:95129487
A;Accession: I67432
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-236 <RES>
A;Cross-references: EMBL:U34964; NID:g1004378; PIDN:AAA77687.1; PID:g1004379
C;Superfamily: bcl transforming protein

Query Match 40.4%; Score 408; DB 2; Length 236;
Best Local Similarity 35.8%; Pred. No. 1.8e-30;
Matches 83; Conservative 35; Mismatches 62; Indels 52; Gaps 3;

```
Qy       9 DTRALVADFVGYRLRQKGY---------------------------------------- 27
           | | :|  :: |:| |:||
Db      10 DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRRAPTPGIFSFQPESNRTPAVHRDTAART 69

Qy      28 ------VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                |  |||   |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db      70 SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
```

```
          | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||  :
Db    130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMYPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy    142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
          |||  |  |||       | | : :| |::|:|: |: :|| :|:||:   |
Db    190 GGWDAFVELYG----PSMRPLFDFSWQSLKTLLSLAL-VGACITLGAYLGHK 236


RESULT   8
I53744
gene bcl-2 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C;Accession: I53744
R;Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.
Gene 140, 291-292, 1994
A;Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.
A;Reference number: I53744; MUID:94193015
A;Accession: I53744
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-236 <RES>
A;Cross-references: GB:L14680; NID:g408946; PIDN:AAA53662.1; PID:g408947
C;Genetics:
A;Gene: bcl-2
C;Superfamily: bcl transforming protein


  Query Match             39.9%;  Score 403;  DB 2;  Length 236;
  Best Local Similarity   35.3%;  Pred. No. 5.4e-30;
  Matches   82;  Conservative   35;  Mismatches   63;  Indels   52;  Gaps    3;

Qy      9 DTRALVADFVGYRLRQKGY----------------------------------------- 27
          | | :|  :: |:| |:||
Db     10 DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRAAPTPGIFSFQPESNRTPAVHRDTAART 69

Qy     28 ------VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                |  |||   |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db     70 SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy     82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
          | :|||: | ||||:|||| ||  :|  |||:|| |||  :  ||  ||   |  ||  :
Db    130 VVEELFRDGVNWGRIVAFFEFGGVMCVGSVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy    142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
          |||  |  |||       | | : :| |::|:|: |: :|| :|:||:   |
Db    190 GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236


RESULT   9
TVMSA1
transforming protein bcl-2-alpha - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999
C;Accession: A25960; E37332
R;Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
Cell 49, 455-463, 1987
A;Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homol
A;Reference number: A90893; MUID:87187643
A;Accession: A25960
A;Molecule type: DNA
A;Residues: 1-236 <NEG>
A;Cross-references: GB:L31532; GB:M16506; NID:g468336; PIDN:AAA37282.1; PID:g387109
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
A;Reference number: A37332; MUID:92375724
A;Accession: E37332
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 1-33,'E',34-220,'AL',223-236 <EGU>
C;Genetics:
A;Gene: BCL2
A;Introns: 192/3
C;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane


  Query Match             39.8%;  Score 402;  DB 1;  Length 236;
  Best Local Similarity   36.6%;  Pred. No. 6.7e-30;
  Matches   85;  Conservative   34;  Mismatches   61;  Indels   52;  Gaps    5;

Qy      9 DTRALVADFVGYRLRQKGYVCGAG------------PG---------------------- 34
          | | :|  :: |:| |:||   ||            ||
Db     10 DNREIVMKYIHYKLSQRGYEWDAGDADAAPLGAAPTPGIFSFQPESNPMPAVHREMAART 69

Qy     35 ---------EGPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                   |||  |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db     70 SPLRPLVATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy     82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
          | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||  :
Db    130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy    142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
          |||  |  |||       | | : :| |::|:|:    :|| :|:||:   |
Db    190 GGWDAFVELYG----PSMRPLFDFSWLSLKTLLS-LPWVGACITLGAYLGHK 236


RESULT  10
I67431
BCL-X-Long - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: I67431
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: eq
onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
A;Reference number: I53295; MUID:95129487
A;Accession: I67431
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-233 <RES>
A;Cross-references: EMBL:U34963; NID:g1004376; PIDN:AAA77686.1; PID:g1004377
C;Superfamily: bcl transforming protein


  Query Match             39.8%;  Score 401.5;  DB 2;  Length 233;
  Best Local Similarity   39.1%;  Pred. No. 7.3e-30;
  Matches   88;  Conservative   23;  Mismatches   61;  Indels   53;  Gaps    4;

Qy     11 RALVADFVGYRLRQKGY-----------------------------------------V 28
          | || ||: |:| ||||                                         |
Db      6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAV 65

Qy     29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
            ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:  | |
Db     66 NGA-TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTVYQSFE 124

Qy     81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
          || :|||: | ||||:||   || ||| |||:|||: || ::  ||  ||   |  ||
Db    125 QVVNELFRDGVNWGRIVASSSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy    141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
          :||| |  |||:    |:|: :|    |      : | | ||:|
Db    185 NGGWDTFVDLYGNNTAPESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT  11
JC7383
B-cell lymphoma 2 protein - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 08-Dec-2000
C;Accession: JC7383
R;Tomicic, M.T.; Christmann, M.; Kaina, B.
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Biochem. Biophys. Res. Commun. 275, 899-903, 2000
A;Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
A;Reference number: JC7383
A;Contents: Ovary
A;Accession: JC7383
A;Molecule type: mRNA
A;Residues: 1-236 <TOM>
A;Cross-references: GB:AJ271720
C;Comment: This protein has anti-apoptotic function, and supports cell survival.
C;Genetics:
A;Gene: bcl-2
C;Superfamily: bcl transforming protein
C;Keywords: B-cell lymphoma; ovary


  Query Match             39.5%;  Score 399;  DB 2;  Length 236;
  Best Local Similarity   34.9%;  Pred. No. 1.3e-29;
  Matches   81;  Conservative   35;  Mismatches   64;  Indels   52;  Gaps    3;

Qy       9 DTRALVADFVGYRLRQKGY---------------------------------------- 27
           | | :|  :: |:| |:||
Db      10 DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART 69

Qy      28 ------VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                 |   ||   |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db      70 SPLRPIVATTGPTLSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
           | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||  :
Db     130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy     142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
           |||  |  |||       | | : :| |::|:|: |: :|| :|:| :    |
Db     190 GGWDAFVELYG----PSVRPLFDFSWLSLKTLLSLAL-VGACITLGTYLGHK 236


RESULT  12
A47537
apoptosis regulator bcl-x - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999
C;Accession: A47537
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74, 597-608, 1993
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A;Reference number: A47537; MUID:93364977
A;Accession: A47537
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-190 <BOI>
A;Cross-references: GB:Z23110; GB:L20120; NID:g510898; PIDN:CAA80657.1; PID:g510899
C;Superfamily: bcl transforming protein


  Query Match             37.2%;  Score 375;  DB 2;  Length 190;
  Best Local Similarity   43.2%;  Pred. No. 1.7e-27;
  Matches   80;  Conservative   15;  Mismatches   44;  Indels   46;  Gaps    3;

Qy      11 RALVADFVGYRLRQKGY----------------------VCGAGPGEGP---------- 37
           | || ||| |:| |:|:                      |    |   |
Db       6 RELVIDFVSYKLSQRGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT 65

Qy      38 ------------AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
                       |  : ||:| |||||| |:|| |||| :|||:|||:| | | || :|
Db      66 VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE 125

Qy      86 LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWA 145
           ||  | ||||:|||| || ||| |||:|||  |||::  ||  ||   |  ||  :|||
Db     126 LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWV 185

Qy     146 EFTAL 150
             |||
Db     186 R-TAL 189


RESULT  13
I49057
bcl-x transmembrane deleted - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C;Accession: I49057
R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
J. Immunol. 153, 4388-4398, 1994
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes
A;Reference number: I49055; MUID:95052604
A;Accession: I49057
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-214 <RES>
A;Cross-references: EMBL:U10102; NID:g506649; PIDN:AAA82174.1; PID:g506650
C;Genetics:
A;Gene: bcl-x-long
C;Superfamily: bcl transforming protein


  Query Match             37.1%;  Score 374.5;  DB 2;  Length 214;
  Best Local Similarity   42.2%;  Pred. No. 2.1e-27;
  Matches   79;  Conservative   17;  Mismatches   40;  Indels   51;  Gaps    3;

Qy      11 RALVADFVGYRLRQKGY----------------------------------------V 28
           | || ||: |:| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
           ||  |   : |          : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy     141 SGGWAEF 147
           :|||  |
Db     185 NGGWDTF 191


RESULT  14
JE0203
apoptosis regulator bcl-x isoform - human
N;Alternate names: h-bcl-xbeta
C;Species: Homo sapiens (man)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 16-Jul-1999
C;Accession: JE0203
R;Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler, E.
Biochem. Biophys. Res. Commun. 248, 147-152, 1998
A;Title: Identification of a human cDNA encoding a novel bcl-x isoform.
A;Reference number: JE0203; MUID:98340865
A;Accession: JE0203
A;Molecule type: mRNA
A;Residues: 1-227 <BAN>
A;Cross-references: GB:U72398; NID:g1622940; PIDN:AAB17354.1; PID:g1622941
C;Genetics:
A;Gene: bcl-x
A;Map position: 20
C;Superfamily: bcl transforming protein


  Query Match             36.8%;  Score 371.5;  DB 2;  Length 227;
  Best Local Similarity   40.3%;  Pred. No. 4.3e-27;
  Matches   81;  Conservative   19;  Mismatches   50;  Indels   51;  Gaps    3;

Qy      11 RALVADFVGYRLRQKGY----------------------------------------V 28
           | || ||: |:| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
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          ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db     66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy     81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
          || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db    125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE 184

Qy    141 SGGWAEFTALYGDGALEEARR 161
          :|||      |    :|   :|
Db    185 NGGWVRTKPLVCPFSLASGQR 205


RESULT  15
B37332
transforming protein (bcl-2-beta) - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 24-Apr-1998
C;Accession: B37332; S35452
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
A;Reference number: A37332; MUID:92375724
A;Accession: B37332
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-216 <EGU>
A;Cross-references: EMBL:D11381; EMBL:D11382
C;Superfamily: bcl transforming protein


  Query Match             35.0%;  Score 353;  DB 2;  Length 216;
  Best Local Similarity   37.8%;  Pred. No. 2.1e-25;
  Matches   70;  Conservative   22;  Mismatches   49;  Indels   44;  Gaps    2;

Qy      9 DTRALVADFVGYRLRQKGYVCGAG-------PGEGPAADP------------------- 41
          | | :|  :: |:| |:||   ||       |   ||| |
Db     10 DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPEPPGSA 69

Qy     42 ----------------LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSD 84
                           :| |:| ||||| |::| |: :: |||:|| :|  ||  | :
Db     70 AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE 129

Qy     85 ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGW 144
          |||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   | :||  :|||
Db    130 ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW 189

Qy    145 AEFTA 149
               |
Db    190 VRACA 194


Search completed: June 10, 2002, 10:26:22
Job time: 170 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 10:32:13 ; Search time 15.84 Seconds
(without alignments)
471.772 Million cell updates/sec

Title: US-09-155-327E-9
Perfect score: 1009
Sequence: 1 MATPASTPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1006	99.7	193	1	BCLW_MOUSE	P70345 mus musculu
2	997	98.8	193	1	BCLW_HUMAN	Q92843 homo sapien
3	647.5	64.2	228	1	AR1_XENLA	Q91827 xenopus lae
4	429.5	42.6	229	1	BCLX_CHICK	Q07816 gallus gall
5	428.5	42.5	233	1	BCLX_PIG	O77737 sus scrofa
6	425.5	42.2	233	1	BCLX_MOUSE	Q64373 mus musculu
7	425.5	42.2	233	1	BCLX_RAT	P53563 rattus norv
8	424.5	42.1	233	1	BCLX_HUMAN	Q07817 homo sapien
9	420.5	41.7	233	1	BCL2_CHICK	Q00709 gallus gall
10	412.5	40.9	229	1	BCL2_BOVIN	O02718 bos taurus
11	410	40.6	236	1	BCL2_RAT	P49950 rattus norv
12	409	40.5	236	1	BCL2_MOUSE	P10417 mus musculu
13	408.5	40.5	239	1	BCL2_HUMAN	P10415 homo sapien
14	399	39.5	236	1	BCL2_CRILO	Q9jjv8 cricetulus
15	366	36.3	204	1	AR11_XENLA	Q91828 xenopus lae
16	175.5	17.4	208	1	BAK_MOUSE	O08734 mus musculu
17	174	17.2	211	1	BAK_HUMAN	Q16611 homo sapien
18	169	16.7	211	1	BAK2_HUMAN	Q13014 homo sapien
19	156.5	15.5	192	1	BAXA_MOUSE	Q07813 mus musculu
20	155.5	15.4	192	1	BAXA_RAT	Q63690 rattus norv
21	154	15.3	192	1	BAXA_HUMAN	Q07812 homo sapien
22	154	15.3	280	1	CED9_CAEEL	P41958 caenorhabdi
23	148	14.7	192	1	BAXA_BOVIN	O02703 bos taurus
24	147.5	14.6	218	1	BAXB_HUMAN	Q07814 homo sapien
25	144	14.3	177	1	NR13_COTJA	Q90343 coturnix co
26	140.5	13.9	271	1	CED9_CAEBR	P41957 caenorhabdi
27	138.5	13.7	143	1	BAXD_HUMAN	P55269 homo sapien
28	119	11.8	175	1	BFL1_HUMAN	Q16548 homo sapien
29	116	11.5	350	1	MCL1_HUMAN	Q07820 homo sapien
30	105	10.4	172	1	BFL1_MOUSE	Q07440 mus musculu
31	99.5	9.9	179	1	EAR_ASFM2	Q07819 african swi
32	98.5	9.8	179	1	EAR_ASFB7	P42485 african swi
33	98.5	9.8	179	1	EAR_ASFE4	Q07818 african swi
34	92.5	9.2	658	1	SQHC_BRAJA	P54924 bradyrhizob
35	86.5	8.6	3433	1	POLG_KUNJM	P14335 k genome po
36	84.5	8.4	358	1	GLNA_LACSA	P23712 lactuca sat
37	82.5	8.2	3430	1	POLG_WNV	P06935 w genome po
38	81.5	8.1	886	1	A4_DROME	P14599 drosophila
39	81	8.0	396	1	PORA_PYRFU	Q51804 pyrococcus
40	80.5	8.0	236	1	YJ94_ARCFU	O28285 archaeoglob
41	79	7.8	454	1	YB48_MYCTU	O06548 mycobacteri
42	79	7.8	454	1	YJ45_MYCTU	P95269 mycobacteri
43	77.5	7.7	1440	1	POLG_JAEVN	P14403 j genome po
44	77.5	7.7	3432	1	POLG_JAEVJ	P32886 j genome po
45	77	7.6	162	1	PHCA_SYNP6	P00308 synechococc

ALIGNMENTS

RESULT 1
BCLW_MOUSE
ID BCLW_MOUSE STANDARD; PRT; 193 AA.
AC P70345;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Apoptosis regulator Bcl-W.
GN BCL2L2 OR BCLW.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358615; PubMed=8761287;
RA Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;
RT "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
RL Oncogene 13:665-675(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/10J;
RX MEDLINE=98160183; PubMed=9500547;
RA Ross A.J., Waymire K.G., Moss J.E., Parlow A.F., Skinner M.K.,
RA Russell L.D., Macgregor G.R.;
RT "Testicular degeneration in Bclw-deficient mice.";
RL Nat. Genet. 18:251-256(1998).
CC -!- FUNCTION: PROMOTES CELL SURVIVAL.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND
CC IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,
CC AND SALIVARY GLAND.
CC -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC FUNCTION.
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC ----------

CC ----------
DR EMBL; U59746; AAB09056.1; -.
DR EMBL; AF030769; AAB86430.1; -.
DR HSSP; Q07817; 1MAZ.
DR MGD; MGI:108052; Bcl2l2.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR003093; BH4.
DR InterPro; IPR000712; Bcl_2.
DR Pfam; PF00452; Bcl-2; 1.

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DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis.
FT   DOMAIN        9     29       BH4.
FT   DOMAIN       85    104       BH1.
FT   DOMAIN      136    151       BH2.
SQ   SEQUENCE   193 AA;  20790 MW;  36CA185F5945DFB4 CRC64;


  Query Match           99.7%;  Score 1006;  DB 1;  Length 193;
  Best Local Similarity   99.5%;  Pred. No. 1.8e-82;
  Matches  192;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db       1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy     121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 GALVTVGAFFASK 193


RESULT   2
BCLW_HUMAN
ID   BCLW_HUMAN     STANDARD;      PRT;   193 AA.
AC   Q92843;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Apoptosis regulator Bcl-W.
GN   BCL2L2 OR BCLW OR KIAA0271.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96358615; PubMed=8761287;
RA   Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,
RA   Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;
RT   "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
RL   Oncogene 13:665-675(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97191544; PubMed=9039502;
RA   Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,
RA   Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
RT   "Prediction of the coding sequences of unidentified human genes. VI.
RT   The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
RT   analysis of cDNA clones from cell line KG-1 and brain.";
RL   DNA Res. 3:321-329(1996).
CC   -!- FUNCTION: PROMOTES CELL SURVIVAL.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND
CC       IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,
CC       AND SALIVARY GLAND.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION.
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U59747; AAB09055.1; -.
DR   EMBL; D87461; BAA19666.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   MIM; 601931; -.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis.
FT   DOMAIN        9     29       BH4.
FT   DOMAIN       85    104       BH1.
FT   DOMAIN      136    151       BH2.
SQ   SEQUENCE   193 AA;  20774 MW;  3792243A50281761 CRC64;


  Query Match           98.8%;  Score 997;  DB 1;  Length 193;
  Best Local Similarity   98.4%;  Pred. No. 1.1e-81;
  Matches  190;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           |||||| ||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db       1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy     121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 GALVTVGAFFASK 193


RESULT   3
AR1_XENLA
ID   AR1_XENLA      STANDARD;      PRT;   228 AA.
AC   Q91827;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Apoptosis regulator R1 (XR1) (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Head;
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RX   MEDLINE=95331613; PubMed=7607538;
RA   Cruz-Reyes J., Tata J.R.;
RT   "Cloning, characterization and expression of two Xenopus bcl-2-like
RT   cell-survival genes.";
RL   Gene 158:171-179(1995).
CC   -!- FUNCTION: COULD BE THE HOMOLOG OF MAMMALIAN BCL-W.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC   -!- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
CC       BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND
CC       ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X82462; CAA57845.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
KW   Apoptosis; Transmembrane.
FT   NON_TER       1      1
FT   DOMAIN      120    139       BH1.
FT   DOMAIN      171    186       BH2.
FT   TRANSMEM    207    227       POTENTIAL.
SQ   SEQUENCE   228 AA;  25068 MW;  C499D449A585F8A9 CRC64;
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  Query Match             64.2%;  Score 647.5;  DB 1;  Length 228;
  Best Local Similarity   67.9%;  Pred. No. 1.4e-50;
  Matches  125;  Conservative   21;  Mismatches   35;  Indels    3;  Gaps    1;

Qy      10 TRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLH 69
           :|||| | | |:| |:  |       | |:  || |||||||||| |||: ||::: |:|
Db      48 SRALVEDLVRYKLCQRSLV---PEPSGAASCALHSAMRAAGDEFEERFRQAFSEISTQIH 104

Qy      70 VTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAY 129
           ||||:|  || :|:  ||||| ||||:|||||||||||||||||||| ||: ::||||| |
Db     105 VTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDWMVTY 164

Qy     130 LETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAF 189
           ||| | ||| |:|||  |  ||||||:||||| |||||||::||||||||||||:||||
Db     165 LETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGALMTVGAL 224

Qy     190 FASK 193
           ||||
Db     225 FASK 228
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RESULT   4
BCLX_CHICK
ID   BCLX_CHICK     STANDARD;      PRT;   229 AA.
AC   Q07816; Q98908;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Apoptosis regulator Bcl-X.
GN   BCL2L1 OR BCLX OR BCL-X.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A. (SHORT FORM).
RX   MEDLINE=93364977; PubMed=8358789;
RA   Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA   Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT   "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT   of apoptotic cell death.";
RL   Cell 74:597-608(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (LONG FORM).
RC   STRAIN=HUBBARD WHITE MOUNTAIN; TISSUE=Testis;
RX   MEDLINE=97264485; PubMed=9110311;
RA   Vilagrasa X., Mezquita C., Mezquita J.;
RT   "Differential expression of bcl-2 and bcl-x during chicken
RT   spermatogenesis.";
RL   Mol. Reprod. Dev. 47:26-29(1997).
CC   -!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC       FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT
CC       ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC       ENVELOPE (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC       SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID
CC       DEVELOPMENT.
CC   -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC       FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC       APOPTOTIC ACTIVITY (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Z23110; CAA80657.1; -.
DR   EMBL; U26645; AAB07677.1; -.
DR   PIR; A47537; A47537.
DR   HSSP; P53563; 1AF3.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Transmembrane; Alternative splicing.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       82     96       BH3.
FT   DOMAIN      125    144       BH1.
FT   DOMAIN      176    191       BH2.
FT   TRANSMEM    206    223       POTENTIAL.
FT   VARSPLIC    185    229       ERFVDLYGNNAAAELRKGQETFNKWLLTGATVAGVLLLGSL
FT                                LSRK -> VRTALP (IN SHORT ISOFORM).
SQ   SEQUENCE   229 AA;  25733 MW;  A97D3A4D04C0E9DA CRC64;
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  Query Match             42.6%;  Score 429.5;  DB 1;  Length 229;
  Best Local Similarity   41.2%;  Pred. No. 3.3e-31;
  Matches   94;  Conservative   23;  Mismatches   62;  Indels   49;  Gaps    4;

Qy      11 RALVADFVGYRLRQKGY----------------------VCGAGPGEGP---------- 37
           | || ||| |:| |:|:                      |   |   |
Db       6 RELVIDFVSYKLSQRGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT 65

Qy      38 ------------AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
                       |  : ||:| |||||| |:|| |||| :|||:|||:| | | || :|
Db      66 VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE 125

Qy      86 LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWA 145
           ||  | ||||:|||| || ||| |||:||| |||::  ||  ||   |  ||  :|||
Db     126 LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWE 185

Qy     146 EFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
            |  |||: |   |  ||:|     : :||||   | |: :|:  : |
Db     186 RFVDLYGNNA---AAELRKGQETFNKWLLTGATVAGVLL-LGSLLSRK 229


RESULT   5
BCLX_PIG
ID   BCLX_PIG       STANDARD;      PRT;   233 AA.
AC   O77737;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Apoptosis regulator Bcl-x.
GN   BCL2L1 OR BLC2L OR BCLX.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT   "Expression of apoptosis-associated genes in hibernating and stunned
RT   myocardium of pig.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC       caspases (By similarity). Appears to regulate cell death by
CC       blocking the volatage-dependent anion channnel (VDAC) by binding
CC       to it and preventing the release of the caspase activator,
CC       cytochrome c, from the mitochondrial membrane.
CC   -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC       similarity). Heterodimerization with BAX does not seem to be
CC       required for anti-apoptotic activity (By similarity).
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC       ENVELOPE (BY SIMILARITY).
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC       The BH1 and BH2 domains are required for both heterodimerization
CC       with other Bcl2 family members and for repression of cell death.
CC   -!- PTM: Proteolytically cleaved by caspases during apoptosis (By
CC       similarity). The cleaved protein, lacking the BH4 domain, has pro-
CC       apoptotic activity (By similarity).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ001203; CAA04597.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Mitochondrion; Transmembrane.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       86    100       BH3.
FT   DOMAIN      129    148       BH1.
FT   DOMAIN      180    195       BH2.
FT   TRANSMEM    210    226       POTENTIAL.
SQ   SEQUENCE   233 AA;  26061 MW;  18BF6FA0441912B2 CRC64;


  Query Match             42.5%;  Score 428.5;  DB 1;  Length 233;
  Best Local Similarity   41.3%;  Pred. No. 4.1e-31;
  Matches   93;  Conservative   22;  Mismatches   57;  Indels   53;  Gaps    4;

Qy      11 RALVADFVGYRLRQKGY-----------------------------------------V 28
           | || ||: |:| ||||                                         |
Db       6 RELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVLNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQE 184

Qy     141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           :|||  |  |||: |  |:|: :|    |      | | | ||:|
Db     185 NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTLAGVVLLGSL 229


RESULT   6
BCLX_MOUSE
ID   BCLX_MOUSE     STANDARD;      PRT;   233 AA.
AC   Q64373; Q60657; Q60658; Q61338;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Apoptosis regulator Bcl-x.
GN   BCL2L1 OR BCL2L OR BCLX.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=2A4B;
RA   Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;
RL   Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=95331139; PubMed=7607090;
RA   Gonzalez-Garcia M., Perez-Ballestero R., Ding L., Duan L., Boise L.H.,
RA   Thompson C.B., Nunez G.;
RT   "bcl-XL is the major bcl-x mRNA form expressed during murine
RT   development and its product localizes to mitochondria.";
RL   Development 120:3033-3042(1994).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS X(L); X(S) AND X(DELTA-TM)).
RC   TISSUE=Pre-B cell;
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RX   MEDLINE=95052604; PubMed=7963517;
RA   Fang W., Rivard J.J., Mueller D.L., Behrens T.W.;
RT   "Cloning and molecular characterization of mouse bcl-x in B and T
RT   lymphocytes.";
RL   J. Immunol. 153:4388-4398(1994).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM X(BETA)).
RC   STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX   MEDLINE=98051053; PubMed=9390687;
RA   Yang X.-F., Weber G.F., Cantor H.;
RT   "A novel Bcl-x isoform connected to the T cell receptor regulates
RT   apoptosis in T cells.";
RL   Immunity 7:629-639(1997).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97289584; PubMed=9144489;
RA   Grillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N.,
RA   Ohta S., Seldin M.F., Nunez G.;
RT   "Genomic organization, promoter region analysis, and chromosome
RT   localization of the mouse bcl-x gene.";
RL   J. Immunol. 158:4750-4757(1997).
CC   -!- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC       caspases (By similarity). Appears to regulate cell death by
CC       blocking the volatage-dependent anion channnel (VDAC) by binding
CC       to it and preventing the release of the caspase activator,
CC       cytochrome c, from the mitochondrial membrane. The Bcl-x(S)
CC       isoform promotes apoptosis.
CC   -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC       similarity). Heterodimerization with BAX does not seem to be
CC       required for anti-apoptotic activity (By similarity).
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC       ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELTA-TM).
CC   -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; BCX-X(L) (SHOWN HERE), BCL-X(S),
CC       BCL-X(BETA) AND BCL-X(DELTA-TM); ARE PRODUCED BY ALTERNATIVE
CC       SPLICING.
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN THE
CC       BRAIN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA-
CC       TM) EXPRESSION IS ENHANCED IN B AND T LYMPHOCYTES THAT HAVE BEEN
CC       ACTIVATED.
CC   -!- DEVELOPMENTAL STAGE: BCL-X(BETA)IS EXPRESSED IN BOTH EMBRYONAL AND
CC       POSTNATAL TISSUES, WHEREAS BCL-X(L) IS PREDOMINANTLY FOUND IN
CC       POSTNATAL TISSUES.
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC       The BH1 and BH2 domains are required for both heterodimerization
CC       with other Bcl2 family members and for repression of cell death.
CC   -!- PTM: Proteolytically cleaved by caspases during apoptosis (By
CC       similarity). The cleaved protein, lacking the BH4 domain, has pro-
CC       apoptotic activity (By similarity).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X83574; CAA58557.1; -.
DR   EMBL; L35049; AAA51039.1; -.
DR   EMBL; L35048; AAA51040.1; -.
DR   EMBL; U10102; AAA82174.1; -.
DR   EMBL; U10101; AAA82173.1; -.
DR   EMBL; U10100; AAA82172.1; -.
DR   EMBL; U51279; AAC53460.1; -.
DR   EMBL; U78031; AAB96881.1; -.
DR   EMBL; U78030; AAB96881.1; JOINED.
DR   HSSP; P53563; 1AF3.
DR   MGD; MGI:88139; Bcl2l.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       86    100       BH3.
FT   DOMAIN      129    148       BH1.
FT   DOMAIN      180    195       BH2.
FT   TRANSMEM    210    226       POTENTIAL.
FT   VARSPLIC    126    188       MISSING (IN ISOFORM BCL-X(S)).
FT   VARSPLIC    189    233       DTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
FT                                FSRK -> VRTTPLVCPPLACVSLLCEHP (IN ISOFORM
FT                                BCL-X(BETA)).
FT   VARSPLIC    194    233       LYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSLFSRK
FT                                -> GHDCGWCGSAGLTLQSEVTRH (IN ISOFORM BCL-
FT                                X(DELTA-TM)).
SQ   SEQUENCE   233 AA;  26132 MW;  24D2AC79887E072E CRC64;


  Query Match             42.2%;  Score 425.5;  DB 1;  Length 233;
  Best Local Similarity   40.9%;  Pred. No. 7.5e-31;
  Matches   92;  Conservative   23;  Mismatches   57;  Indels   53;  Gaps    4;

Qy      11 RALVADFVGYRLRQKGY----------------------------------------V 28
           | || ||: |:| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy     141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           :|||  |  |||: |  |:|: :|    |      : | | ||:|
Db     185 NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT   7
BCLX_RAT
ID   BCLX_RAT       STANDARD;      PRT;   233 AA.
AC   P53563; Q62678; P70614; P70613; Q62836; Q64087; Q64128;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Apoptosis regulator Bcl-x.
GN   BCL2L1 OR BLC2L OR BCLX.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RC   TISSUE=Brain;
RA   Michaelidis T.M.;
RL   Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Wesselingh S.L., David G.L., Choi S., Veliuona M., Hardwick J.M.;
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
RC   TISSUE=Thymus;
RX   MEDLINE=96278736; PubMed=8662675;
RA   Shiraiwa N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Ohta S.;
RT   "An additional form of rat Bcl-x, Bcl-xbeta, generated by an
RT   unspliced RNA, promotes apoptosis in promyeloid cells.";
RL   J. Biol. Chem. 271:13258-13265(1996).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Ovary;
RX   MEDLINE=95129487; PubMed=7828536;
RA   Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
RT   "Expression of members of the bcl-2 gene family in the immature rat
RT   ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT   cell apoptosis is associated with decreased bax and constitutive
RT   bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
RL   Endocrinology 136:232-241(1995).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX   MEDLINE=98010630; PubMed=9346936;
RA   Aritomi M., Kunishima N., Inohara N., Ishibashi Y., Ohta S.,
RA   Morikawa K.;
RT   "Crystal structure of rat Bcl-xL. Implications for the function of
RT   the Bcl-2 protein family.";
RL   J. Biol. Chem. 272:27886-27892(1997).
CC   -!- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC       caspases (By similarity). Appears to regulate cell death by
CC       blocking the volatage-dependent anion channnel (VDAC) by binding
CC       to it and preventing the release of the caspase activator,
CC       cytochrome c, from the mitochondrial membrane. The Bcl-x(S) and
CC       Bcl-x(beta) isoforms promote apoptosis.
CC   -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC       similarity). Heterodimerization with BAX does not seem to be
CC       required for anti-apoptotic activity (By similarity).
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC       ENVELOPE (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S)
CC       AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS
CC       SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE
CC       OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT
CC       DETECTABLE LEVEL OF BCL-X(S).
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC       The BH1 and BH2 domains are required for both heterodimerization
CC       with other Bcl2 family members and for repression of cell death.
CC   -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC       cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC       activity (By similarity).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X82537; CAA57886.1; -.
DR   EMBL; X82537; CAA57887.1; -.
DR   EMBL; U10579; AAA19257.1; -.
DR   EMBL; U72350; AAB17353.1; -.
DR   EMBL; U72349; AAB17352.1; -.
DR   EMBL; U34963; AAA77686.1; -.
DR   EMBL; S76513; AAC60701.1; ALT_INIT.
DR   EMBL; S78284; AAC60702.1; -.
DR   PDB; 1AF3; 07-JUL-97.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
KW   3D-structure.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       86    100       BH3.
FT   DOMAIN      129    148       BH1.
FT   DOMAIN      180    195       BH2.
FT   TRANSMEM    210    226       POTENTIAL.
FT   VARSPLIC    126    188       MISSING (IN ISOFORM BCL-X(S)).
FT   VARSPLIC    189    233       DTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
FT                                FSRK -> VRTTPLVCPPLVCLSSVEIPNCPFWSPGMVVED
FT                                IDYSGDIPGLL (IN ISOFORM BCL-X(BETA)).
FT   CONFLICT      6      6       R -> Q (IN REF. 1).
FT   CONFLICT     12     12       F -> S (IN REF. 2).
FT   CONFLICT     64     64       A -> E (IN REF. 2).
FT   CONFLICT     81     81       I -> L (IN REF. 4).
FT   CONFLICT    119    119       A -> V (IN REF. 4).
FT   CONFLICT    143    144       FF -> SS (IN REF. 4).
FT   CONFLICT    199    199       A -> T (IN REF. 4).
FT   CONFLICT    201    201       A -> P (IN REF. 4).
SQ   SEQUENCE   233 AA;  26158 MW;  2B62B6C63864BC8F CRC64;


  Query Match             42.2%;  Score 425.5;  DB 1;  Length 233;
  Best Local Similarity   40.9%;  Pred. No. 7.5e-31;
  Matches   92;  Conservative   23;  Mismatches   57;  Indels   53;  Gaps    4;

Qy      11 RALVADFVGYRLRQKGY----------------------------------------V 28
           | || ||: |:| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |        : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy     141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           :|||  |  |||: |  |:|: :|    |      : | | ||:|
Db     185 NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT   8
BCLX_HUMAN
ID   BCLX_HUMAN     STANDARD;      PRT;   233 AA.
AC   Q07817; Q92976;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Apoptosis regulator Bcl-x.
GN   BCL2L1 OR BCL2L OR BCLX.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RX   MEDLINE=93364977; PubMed=8358789;
RA   Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA   Turka L.A., Mao X., Nunez G., Thompson C.B.;
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RT   "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT   of apoptotic cell death.";
RL   Cell 74:597-608(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM BETA).
RA   Inohara N., Ohta S.;
RL   Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.
RX   MEDLINE=95372373; PubMed=7644501;
RA   Sedlak T.W., Oltvai Z.N., Yang E., Wang K., Boise L.H., Thompson C.B.,
RA   Korsmeyer S.J.;
RT   "Multiple Bcl-2 family members demonstrate selective dimerizations
RT   with Bax.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).
RN   [4]
RP   MUTAGENESIS OF BH1 AND BH2 DOMAINS.
RX   MEDLINE=96170038; PubMed=8596636;
RA   Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.B., Hardwick J.M.,
RA   Korsmeyer S.J.;
RT   "Bax-independent inhibition of apoptosis by Bcl-XL.";
RL   Nature 379:554-556(1996).
RN   [5]
RP   STRUCTURE BY NMR OF 1-209.
RX   MEDLINE=97172562; PubMed=9020082;
RA   Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J.E.,
RA   Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
RA   Thompson C.B., Fesik S.W.;
RT   "Structure of Bcl-xL-Bak peptide complex: recognition between
RT   regulators of apoptosis.";
RL   Science 275:983-986(1997).
RN   [6]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.
RX   MEDLINE=96256675; PubMed=8692274;
RA   Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,
RA   Yoon H.S., Nettesheim D., Chang B.S., Thompson C.B., Wong S.L.,
RA   Ng S.L., Fesik S.W.;
RT   "X-ray and NMR structure of human Bcl-xL, an inhibitor of programmed
RT   cell death.";
RL   Nature 381:335-341(1996).
RN   [7]
RP   CLEAVAGE BY CASPASES, AND MUTAGENESIS OF ASP-61.
RX   MEDLINE=98118550; PubMed=9435230;
RA   Clem R.J., Cheng E.H.-Y., Karp C.L., Kirsch D.G., Ueno K.,
RA   Takahashi A., Kastan M.B., Griffin D.E., Earnshaw W.C., Veliuona M.A.,
RA   Hardwick J.M.;
RT   "Modulation of cell death bx Bcl-xL through caspase interaction.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).
CC   -!- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
CC       caspases (By similarity). Appears to regulate cell death by
CC       blocking the volatage-dependent anion channnel (VDAC) by binding
CC       to it and preventing the release of the caspase activator,
CC       cytochrome c, from the mitochondrial membrane. The Bcl-x(S)
CC       isoform promotes apoptosis.
CC   -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2.
CC       Heterodimerization with BAX does not seem to be required for anti-
CC       apoptotic activity.
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC       ENVELOPE (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S)
CC       AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS
CC       THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING
CC       LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING
CC       LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC       The BH1 and BH2 domains are required for both heterodimerization
CC       with other Bcl2 family members and for repression of cell death.
CC   -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC       cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC       activity.
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ---------------------------------------------------------------------
DR   EMBL; Z23116; CAA80662.1; -.
DR   EMBL; Z23115; CAA80661.1; -.
DR   EMBL; U72398; AAB17354.1; -.
DR   PDB; 1BXL; 29-OCT-97.
DR   PDB; 1LXL; 21-APR-97.
DR   PDB; 1MAZ; 21-APR-97.
DR   MIM; 600039; -.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;
KW   3D-structure.
FT   DOMAIN        4     24       BH4.
FT   DOMAIN       86    100       BH3.
FT   DOMAIN      129    148       BH1.
FT   DOMAIN      180    195       BH2.
FT   TRANSMEM    210    226       POTENTIAL.
FT   SITE         61     61       CLEAVAGE BY CASPASE-1.
FT   VARSPLIC    126    188       MISSING (IN ISOFORM BCL-X(S)).
FT   VARSPLIC    189    233       DTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
FT                                FSRK -> VRTKPLVCPFSLASGQRSPTALLLYLFLLCWVI
FT                                VGDVDS (IN ISOFORM BCL-X(BETA)).
FT   MUTAGEN      61     61       D->A: NO CLEAVAGE BY CASPASE-1 NOR BY
FT                                CASPASE-3.
FT   MUTAGEN      131    133      FRD->VRA: NO HETERODIMERIZATION WITH BAX.
FT   MUTAGEN      135    137      VNW->AIL: LOSS OF ANTI-APOPTOTIC
FT                                ACTIVITY.
FT   MUTAGEN      138    140      GRI->ELN: LOSS OF ANTI-APOPTOTIC
FT                                ACTIVITY.
FT   MUTAGEN      138    138      G->A: NO HETERODIMERIZATION WITH BAX.
FT   MUTAGEN      148    148      G->E: NO HETERODIMERIZATION WITH BAX.
FT   MUTAGEN      156    156      D->A: NO EFECT ON CASPASE-1 CLEAVAGE.
FT   MUTAGEN      176    176      D->A: NO EFECT ON CASPASE-1 CLEAVAGE.
FT   MUTAGEN      188    189      WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY
FT                                BY ABOUT HALF.
FT   MUTAGEN      189    189      D->A: NO EFECT ON CASPASE-1 CLEAVAGE.
FT   CONFLICT      70     70      G -> A (IN REF. 1; CAA80661).
SQ   SEQUENCE   233 AA;  26049 MW;  E09D3CDD851AE9BE CRC64;


  Query Match             42.1%;  Score 424.5;  DB 1;  Length 233;
  Best Local Similarity   40.9%;  Pred. No. 9.2e-31;
  Matches   92;  Conservative   23;  Mismatches   57;  Indels   53;  Gaps    4;

Qy      11 RALVADFVGYRLRQKGY----------------------------------------V 28
           | || ||: |:| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
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Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE 184

Qy     141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           :|||  |  |||: |  |:|: :|    |      : | | ||:|
Db     185 NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT   9
BCL2_CHICK
ID   BCL2_CHICK     STANDARD;      PRT;   233 AA.
AC   Q00709;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Apoptosis regulator Bcl-2.
GN   BCL2 OR BCL-2.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92375724; PubMed=1508712;
RA   Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT   "Isolation and characterization of the chicken bcl-2 gene: expression
RT   in a variety of tissues including lymphoid and neuronal organs in
RT   adult and embryo.";
RL   Nucleic Acids Res. 20:4187-4192(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell lymphoma;
RX   MEDLINE=92379084; PubMed=1511008;
RA   Cazals-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;
RT   "Molecular cloning and DNA sequence analysis of cDNA encoding chicken
RT   homologue of the Bcl-2 oncoprotein.";
RL   Biochim. Biophys. Acta 1132:109-113(1992).
CC   -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC       including factor-dependent lymphohematopoietic and neural cells.
CC       Regulates cell death by controlling the mitochondrial membrane
CC       permeability. Appears to function in a feedback loop system with
CC       caspases. Inhibits caspase activity either by preventing the
CC       release of cytochrome c from the mitochondria and/or by binding to
CC       the apoptosis-activating factor (APAF-1).
CC   -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC       Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC       domains, and is necessary for anti-apoptotic activity (By
CC       similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC       membrane of the nuclear envelope and the endoplasmic reticulum.
CC   -!- TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen,
CC       kidney, heart, ovary and brain, with the highest levels in the
CC       thymus. In the embryo, highly levels expressed in all tissues with
CC       high levels in the bursa of Fabricius.
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC       for interaction with RAF-1 (By similarity).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; D11382; BAA01978.1; -.
DR   EMBL; D11381; BAA01978.1; JOINED.
DR   EMBL; Z11961; CAA78018.1; -.
DR   PIR; A37332; A37332.
DR   PIR; S24390; S24390.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Transmembrane; Mitochondrion.
FT   DOMAIN       10     30       BH4.
FT   DOMAIN       87    101       BH3.
FT   DOMAIN      130    149       BH1.
FT   DOMAIN      181    196       BH2.
FT   TRANSMEM    208    228       POTENTIAL.
FT   CONFLICT     64     64       E -> S (IN REF. 2).
FT   CONFLICT     67     82       GSAAASEVPPAEGLRP -> ARLLLVRCPRLRGCA
FT                                (IN REF. 2).
FT   CONFLICT    121    121       H -> T (IN REF. 2).
FT   CONFLICT    139    139       G -> V (IN REF. 2).
SQ   SEQUENCE   233 AA;  25687 MW;  5252555ACB6E4C3D CRC64;


  Query Match             41.7%;  Score 420.5;  DB 1;  Length 233;
  Best Local Similarity   37.6%;  Pred. No. 2.1e-30;
  Matches   86;  Conservative   33;  Mismatches   61;  Indels   49;  Gaps    4;

Qy       9 DTRALVADFVGYRLRQKGYVCGAG-------PGEGPAADP------------------- 41
           | | :|  :: |:| |:||   ||       |   ||| |
Db      10 DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPEPPGSA 69

Qy      42 ----------------LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSD 84
                           :| |:| |||||  |::| |: :: |||:|| :|  ||  | :
Db      70 AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE 129

Qy      85 ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGW 144
           |||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   | :||  :|||
Db     130 ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW 189

Qy     145 AEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
             | |||:      | | : :| |::|:|:  | :|| :|:||:   |
Db     190 DAFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK 233


RESULT  10
BCL2_BOVIN
ID   BCL2_BOVIN     STANDARD;      PRT;   229 AA.
AC   O02718;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Apoptosis regulator Bcl-2.
GN   BCL2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HOLSTEIN; TISSUE=Thymus;
RA   Reyes R.A., Cockerell G.L.;
RT   "Bovine leukemia virus associated-leukemogenesis is correlated
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RT   with suppression of programmed cell death and increased expression
RT   of Bcl-2.";
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC       including factor-dependent lymphohematopoietic and neural cells.
CC       Regulates cell death by controlling the mitochondrial membrane
CC       permeability. Appears to function in a feedback loop system with
CC       caspases. Inhibits caspase activity either by preventing the
CC       release of cytochrome c from the mitochondria and/or by binding to
CC       the apoptosis-activating factor (APAF-1) (By similarity).
CC   -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC       Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC       domains, and is necessary for anti-apoptotic activity (By
CC       similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC       membrane of the nuclear envelope and the endoplasmic reticulum (By
CC       similarity).
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC       for interaction with RAF-1 (By similarity).
CC   -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC       anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC       on Ser-70 by PKC is required for the anti-apoptosis activity and
CC       occurs during the G2/M phase of the cell cycle(By similarity). In
CC       the absence of growth factors, Bcl2 appears to be phosphorylated
CC       by other protein kinases such as ERKs and stress-activated
CC       kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC       cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC       activity, causes the release of cytochrome c into the cytosol
CC       promoting further caspase activity (By similarity).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U92434; AAB53319.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
FT   DOMAIN       10     30       BH4.
FT   DOMAIN       64     68       POLY-PRO.
FT   DOMAIN       69     72       POLY-ALA.
FT   DOMAIN       83     97       BH3.
FT   DOMAIN      126    145       BH1.
FT   DOMAIN      177    192       BH2.
FT   TRANSMEM    202    223       POTENTIAL.
FT   SITE          34     35       CLEAVAGE (BY CASPASES) (BY SIMILARITY).
FT   MOD_RES       63     63       PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SQ   SEQUENCE   229 AA;  25099 MW;  AD1DD0AF98FFF11D CRC64;
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  Query Match             40.9%;  Score 412.5;  DB 1;  Length 229;
  Best Local Similarity   37.8%;  Pred. No. 1.1e-29;
  Matches   85;  Conservative   36;  Mismatches   59;  Indels   45;  Gaps    5;

Qy       9 DTRALVADFVGYRLRQKGYVCGAG------------------PGE------------- 35
           | | :|  :: |:| |:||   ||                    ||
Db      10 DNREIVMKYIHYKLSQRGYEWDAGDAGAAPPGAAPAPGILSSQPGRTPAPSRTSPPPPPA 69

Qy      36 ---GPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQ 88
              |||  |    :|  :| |||:|  |:|| |::::|||:|| :|::||  | :|||:
Db      70 AAAGPAPSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARERFATVVEELFR 129

Qy      89 GGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFT 148
           | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||  :||| |
Db     130 DGVNWGRIVAFFEFGGVMCVESVNREMSPLVDSIALWMTEYLNRHLHTWIQDNGGWDAFV 189

Qy     149 ALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
           |||       | | : :| |:: :|: |: :|| :|:||:   |
Db     190 ELYG----PSMRPLFDFSWLSLKALLSLAL-VGACITLGAYLGHK 229
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RESULT  11
BCL2_RAT
ID   BCL2_RAT       STANDARD;      PRT;   236 AA.
AC   P49950; Q62837; Q64032;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Apoptosis regulator Bcl-2.
GN   BCL2 OR BCL-2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=94193015; PubMed=8144041;
RA   Sato T., Irie S., Krajewski S., Reed J.C.;
RT   "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
RL   Gene 140:291-292(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Ovary;
RX   MEDLINE=95129487; PubMed=7828536;
RA   Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
RT   "Expression of members of the bcl-2 gene family in the immature rat
RT   ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT   cell apoptosis is associated with decreased bax and constitutive
RT   bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
RL   Endocrinology 136:232-241(1995).
RN   [3]
RP   SEQUENCE OF 19-172 FROM N.A.
RX   MEDLINE=95059917; PubMed=7969891;
RA   Castren E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H.,
RA   Lindholm D.;
RT   "bcl-2 messenger RNA is localized in neurons of the developing and
RT   adult rat brain.";
RL   Neuroscience 61:165-177(1994).
CC   -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC       including factor-dependent lymphohematopoietic and neural cells.
CC       Regulates cell death by controlling the mitochondrial membrane
CC       permeability. Appears to function in a feedback loop system with
CC       caspases. Inhibits caspase activity either by preventing the
CC       release of cytochrome c from the mitochondria and/or by binding to
CC       the apoptosis-activating factor (APAF-1).
CC   -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC       Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC       domains, and is necessary for anti-apoptotic activity (By
CC       similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC       membrane of the nuclear envelope and the endoplasmic reticulum.
CC   -!- TISSUE SPECIFICITY: Expressed in a variety of tissues, with
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CC       highest levels in reproductive tissues. In the adult brain,
CC       expression is localized in mitral cells of the olfactory bulb,
CC       granule and pyramidal neurons of hippocampus, pontine nuclei,
CC       cerebellar granule neurons, and in ependymal cells. In prenatal
CC       brain, expression is higher and localized in the neuroepithelium
CC       and in the cortical plate.
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC       for interaction with RAF-1 (By similarity).
CC   -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC       anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC       on Ser-70 by PKC is required for the anti-apoptosis activity and
CC       occurs during the G2/M phase of the cell cycle. In the absence of
CC       growth factors, Bcl2 appears to be phosphorylated by other protein
CC       kinases such as ERKs and stress-activated kinases.
CC       Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC       cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC       activity, causes the release of cytochrome c into the cytosol
CC       promoting further caspase activity (By similarity).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L14680; AAA53662.1; -.
DR   EMBL; U34964; AAA77687.1; -.
DR   EMBL; S74122; -; NOT_ANNOTATED_CDS.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
FT   DOMAIN       10     30       BH4.
FT   DOMAIN       90    104       BH3.
FT   DOMAIN      133    152       BH1.
FT   DOMAIN      184    199       BH2.
FT   TRANSMEM    209    230       POTENTIAL.
FT   SITE          34     35       CLEAVAGE (BY CASPASES) (BY SIMILARITY).
FT   MOD_RES       70     70       PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
FT   CONFLICT      42     42       A -> R (IN REF. 2).
FT   CONFLICT     157    157       E -> G (IN REF. 1).
FT   CONFLICT     164    164       S -> Y (IN REF. 2).
FT   CONFLICT     212    212       L -> Q (IN REF. 2).
SQ   SEQUENCE   236 AA;  26622 MW;  E7688CB9071A872A CRC64;


  Query Match             40.6%;  Score 410;  DB 1;  Length 236;
  Best Local Similarity   35.8%;  Pred. No. 1.8e-29;
  Matches   83;  Conservative   35;  Mismatches   62;  Indels   52;  Gaps    3;

Qy       9 DTRALVADFVGYRLRQKGY---------------------------------------- 27
           | | :|  :: |:| |:||
Db      10 DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRAAPTPGIFSFQPESNRTPAVHRDTAART 69

Qy      28 ------VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                 |  |||   |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db      70 SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
           | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||  :
Db     130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy     142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
           |||  |  |||       | | : :| |::|:|: |: :|| :|:||:   |
Db     190 GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236


RESULT  12
BCL2_MOUSE
ID   BCL2_MOUSE     STANDARD;      PRT;   236 AA.
AC   P10417; P10418;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Apoptosis regulator Bcl-2.
GN   BCL2 OR BCL-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC   STRAIN=BALB/C; TISSUE=Liver;
RX   MEDLINE=87187643; PubMed=3032455;
RA   Negrini M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.;
RT   "Molecular analysis of mbcl-2: structure and expression of the murine
RT   gene homologous to the human gene involved in follicular lymphoma.";
RL   Cell 49:455-463(1987).
RN   [2]
RP   REVISIONS TO 221-222.
RX   MEDLINE=92375724; PubMed=1508712;
RA   Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT   "Isolation and characterization of the chicken bcl-2 gene: expression
RT   in a variety of tissues including lymphoid and neuronal organs in
RT   adult and embryo.";
RL   Nucleic Acids Res. 20:4187-4192(1992).
RN   [3]
RP   PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.
RX   MEDLINE=97277291; PubMed=9115213;
RA   Ito T., Deng X., Carr B., May W.S. Jr.;
RT   "Bcl-2 phosphorylation required for anti-apoptosis function.";
RL   J. Biol. Chem. 272:11671-11673(1997).
RN   [4]
RP   DEPHOSPHORYLATION BY PP2A.
RX   MEDLINE=99069407; PubMed=9852076;
RA   Deng X., Ito T., Carr B., Mumby M., May W.S. Jr.;
RT   "Reversible phosphorylation of Bcl2 following interleukin 3 or
RT   bryostatin 1 is mediated by direct interaction with protein
RT   phosphatase 2A*.";
RL   J. Biol. Chem. 273:34157-34163(1998).
CC   -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC       including factor-dependent lymphohematopoietic and neural cells.
CC       Regulates cell death by controlling the mitochondrial membrane
CC       permeability. Appears to function in a feedback loop system with
CC       caspases. Inhibits caspase activity either by preventing the
CC       release of cytochrome c from the mitochondria and/or by binding to
CC       the apoptosis-activating factor (APAF-1).
CC   -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC       Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC       domains, and is necessary for anti-apoptotic activity (By
CC       similarity). Also interacts with APAF-1 and RAF-1.
CC   -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC       membrane of the nuclear envelope and the endoplasmic reticulum.
CC   -!- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta;
CC       are produced by alternative splicing.
CC   -!- TISSUE SPECIFICITY: Expressed in a variety of tissues.
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
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CC       for interaction with RAF-1.
CC    -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC       anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC       on Ser-70 by PKC is required for the anti-apoptosis activity and
CC       occurs during the G2/M phase of the cell cycle. In the absence of
CC       growth factors, Bcl2 appears to be phosphorylated by other protein
CC       kinases such as ERKs and stress-activated kinases.
CC       Dephosphorylated by protein phosphatase 2A (PP2A).
CC    -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC       cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC       activity, causes the release of cytochrome c into the cytosol
CC       promoting further caspase activity.
CC    -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC    -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC    -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC    -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC    -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC    ----------------------------------------------------------------------
CC    This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC    use by non-profit institutions as long as its content is in no way
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CC    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC    or send an email to license@isb-sib.ch).
CC    ----------------------------------------------------------------------
DR    EMBL; L31532; AAA37282.1; -.
DR    EMBL; M16506; AAA37282.1; JOINED.
DR    EMBL; M16506; AAA37281.1; -.
DR    PIR; A25960; TVMSA1.
DR    PIR; B25960; TVMSB1.
DR    PIR; E37332; E37332.
DR    HSSP; Q07817; 1MAZ.
DR    MGD; MGI:88138; Bcl2.
DR    InterPro; IPR002475; BCL2_family.
DR    InterPro; IPR003093; BH4.
DR    InterPro; IPR000712; Bcl_2.
DR    Pfam; PF00452; Bcl-2; 1.
DR    Pfam; PF02180; BH4; 1.
DR    SMART; SM00337; BCL; 1.
DR    SMART; SM00265; BH4; 1.
DR    PROSITE; PS50062; BCL2_FAMILY; 1.
DR    PROSITE; PS01080; BH1; 1.
DR    PROSITE; PS01258; BH2; 1.
DR    PROSITE; PS01259; BH3; 1.
DR    PROSITE; PS01260; BH4_1; 1.
DR    PROSITE; PS50063; BH4_2; 1.
KW    Apoptosis; Alternative splicing; Transmembrane; Mitochondrion;
KW    Phosphorylation.
FT    DOMAIN       10     30       BH4.
FT    DOMAIN       90    104       BH3.
FT    DOMAIN      133    152       BH1.
FT    DOMAIN      184    199       BH2.
FT    TRANSMEM    209    230       POTENTIAL.
FT    SITE         34     35       CLEAVAGE (BY CASPASES) (BY SIMILARITY).
FT    MOD_RES      70     70       PHOSPHORYLATION (BY PKC).
FT    VARSPLIC    193    236       DAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYL
FT                                 GHK -> VGACLVE (IN ISOFORM BETA).
SQ    SEQUENCE   236 AA;  26425 MW;  AA85EF6B0766BE0A CRC64;


  Query Match             40.5%;  Score 409;  DB 1;  Length 236;
  Best Local Similarity   37.1%;  Pred. No. 2.2e-29;
  Matches   86;  Conservative   35;  Mismatches   59;  Indels   52;  Gaps    5;

Qy       9 DTRALVADFVGYRLRQKGYVCGAG------------PG---------------------- 34
           | | :|  :: |:| |:||   ||            ||
Db      10 DNREIVMKYIHYKLSQRGYEWDAGDADAAPLGAAPTPGIFSFQPESNPMPAVHREMAART 69

Qy      35 ---------EGPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                   |||  |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db      70 SPLRPLVATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
           | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||  :
Db     130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy     142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
           |||  |  |||       | | : :| |::|:|: |: :|| :|:||:   |
Db     190 GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236


RESULT  13
BCL2_HUMAN
ID    BCL2_HUMAN     STANDARD;      PRT;   239 AA.
AC    P10415; P10416; Q16197; Q13842;
DT    01-MAR-1989 (Rel. 10, Created)
DT    01-APR-1993 (Rel. 25, Last sequence update)
DT    01-MAR-2002 (Rel. 41, Last annotation update)
DE    Apoptosis regulator Bcl-2.
GN    BCL2.
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RX    MEDLINE=86259760; PubMed=3523487;
RA    Tsujimoto Y., Croce C.M.;
RT    "Analysis of the structure, transcripts, and protein products of
RT    bcl-2, the gene involved in human follicular lymphoma.";
RL    Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
RN    [2]
RP    REVISIONS TO 96; 110 AND 237.
RX    MEDLINE=92375724; PubMed=1508712;
RA    Eguchi Y., Ewert D.L., Tsujimoto Y.;
RT    "Isolation and characterization of the chicken bcl-2 gene: expression
RT    in a variety of tissues including lymphoid and neuronal organs in
RT    adult and embryo.";
RL    Nucleic Acids Res. 20:4187-4192(1992).
RN    [3]
RP    SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX    MEDLINE=87002488; PubMed=2875799;
RA    Cleary M.L., Smith S.D., Sklar J.;
RT    "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-
RT    2/immunoglobulin transcript resulting from the t(14;18)
RT    translocation.";
RL    Cell 47:19-28(1986).
RN    [4]
RP    SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX    MEDLINE=88196071; PubMed=2834197;
RA    Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S.,
RA    Goldman P., Korsmeyer S.J.;
RT    "Alternative promoters and exons, somatic mutation and deregulation
RT    of the Bcl-2-Ig fusion gene in lymphoma.";
RL    EMBO J. 7:123-131(1988).
RN    [5]
RP    SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS NHL.
RX    MEDLINE=92096610; PubMed=1339299;
RA    Tanaka S., Louie D.C., Kant J.A., Reed J.C.;
RT    "Frequent incidence of somatic mutations in translocated BCL2
RT    oncogenes of non-Hodgkin's lymphomas.";
RL    Blood 79:229-237(1992).
RN    [6]
RP    SUBCELLULAR LOCATION.
RX    MEDLINE=91066924; PubMed=2250705;
RA    Hockenbery D., Nunez G., Milliman C., Schreiber R.D., Korsmeyer S.J.;
RT    "Bcl-2 is an inner mitochondrial membrane protein that blocks
RT    programmed cell death.";
RL    Nature 348:334-336(1990).
RN    [7]
RP    MUTAGENESIS.
RX    MEDLINE=94239528; PubMed=8183370;
RA    Yin X.-M., Oltvai Z.N., Korsmeyer S.J.;
RT    "BH1 and BH2 domains of Bcl-2 are required for inhibition of
RT    apoptosis and heterodimerization with Bax.";
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RL   Nature 369:321-323(1994).
RN   [8]
RP   CLEAVAGE BY CASPASES, AND MUTAGENESIS.
RX   MEDLINE=98057466; PubMed=9395403;
RA   Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,
RA   Ueno K., Hardwick J.M.;
RT   "Conversion of Bcl-2 to a Bax-like death effector by caspases.";
RL   Science 278:1966-1988(1997).
RN   [9]
RP   REVIEW ON PHOSPHORYLATION.
RX   MEDLINE=21260650; PubMed=11368354;
RA   Ruvolo P.P., Deng X., May W.S.;
RT   "Phosphorylation of Bcl2 and regulation of apoptosis.";
RL   Leukemia 15:515-522(2001).
RN   [10]
RP   PHOSPHORYLATION BY ASK1/JNK1.
RX   MEDLINE=20036804; PubMed=10567572;
RA   Yamamoto K., Ichijo H., Korsmeyer S.J.;
RT   "BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal
RT   protein kinase pathway normally activated at G(2)/M.";
RL   Mol. Cell. Biol. 19:8469-8478(1999).
CC   -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC       including factor-dependent lymphohematopoietic and neural cells.
CC       Regulates cell death by controlling the mitochondrial membrane
CC       permeability. Appears to function in a feedback loop system with
CC       caspases. Inhibits caspase activity either by preventing the
CC       release of cytochrome c from the mitochondria and/or by binding to
CC       the apoptosis-activating factor (APAF-1).
CC   -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC       Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC       domains, and is necessary for anti-apoptotic activity (By
CC       similarity). Also interacts with APAF-1 and RAF-1.
CC   -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC       membrane of the nuclear envelope and the endoplasmic reticulum.
CC   -!- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta;
CC       are produced by alternative splicing.
CC   -!- TISSUE SPECIFICITY: Expressed in a variety of tissues.
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC       for interaction with RAF-1.
CC   -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC       anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC       on Ser-70 by PKC is required for the anti-apoptosis activity and
CC       occurs during the G2/M phase of the cell cycle. In the absence of
CC       growth factors, Bcl2 appears to be phosphorylated by other protein
CC       kinases such as ERKs and stress-activated kinases.
CC       Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC       cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC       activity, causes the release of cytochrome c into the cytosol
CC       promoting further caspase activity.
CC   -!- DISEASE: Involved in follicular lymphoma (FL) (also known as type
CC       II chronic lymphatic leukemia) by a chromosomal translocation
CC       t(14;18)(q32;q21) which involves Bcl2 and immunoglobulin gene
CC       regions.
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M13994; AAA51813.1; ALT_SEQ.
DR   EMBL; M13995; AAA51814.1; ALT_SEQ.
DR   EMBL; M14745; AAA35591.1; -.
DR   EMBL; X06487; CAA29778.1; -.
DR   EMBL; S72602; AAD14111.1; ALT_SEQ.
DR   PIR; A29409; TVHUA1.
DR   PIR; B29409; TVHUB1.
DR   PIR; A24428; TVHUBC.
DR   PIR; C37332; C37332.
DR   PIR; D37332; D37332.
DR   HSSP; Q07817; 1MAZ.
DR   MIM; 151430; -.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Proto-oncogene; Apoptosis; Alternative splicing; Transmembrane;
KW   Mitochondrion; Phosphorylation; Chromosomal translocation;
KW   Polymorphism; Disease mutation.
FT   DOMAIN       10     30       BH4.
FT   DOMAIN       93    107       BH3.
FT   DOMAIN      136    155       BH1.
FT   DOMAIN      187    202       BH2.
FT   TRANSMEM    212    233       POTENTIAL.
FT   SITE          34     35       CLEAVAGE (BY CASPASE-3).
FT   MOD_RES       70     70       PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
FT   VARSPLIC     196    239       DAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYL
FT                                 GHK -> VGASGDVS (IN ISOFORM BETA).
FT   VARIANT        7      7       T -> S.
FT                                 /FTId=VAR_000827.
FT   VARIANT       59     59       P -> S (IN NON-HODGKINS-LYMPHOMA; SOMATIC
FT                                 MUTATION).
FT                                 /FTId=VAR_000828.
FT   VARIANT       93     93       V -> I (IN NON-HODGKINS-LYMPHOMA; SOMATIC
FT                                 MUTATION).
FT                                 /FTId=VAR_000829.
FT   MUTAGEN       34     34       D->A: ABOLISHES CLEAVAGE BY CASPASE-3.
FT   MUTAGEN       64     64       D->A: NO EFFECT ON CLEAVAGE BY CASPASE-3.
FT   MUTAGEN      145    145       G->A: NO HETERODIMERIZATION WITH BAX AND
FT                                 LOSS OF ANTI-APOPTOTIC ACTIVITY.
FT   MUTAGEN      188    188       W->A: NO HETERODIMERIZATION WITH BAX AND
FT                                 LOSS OF ANTI-APOPTOTIC ACTIVITY.
FT   CONFLICT      48     48       I -> F (IN REF. 4).
FT   CONFLICT      59     59       P -> T (IN REF. 3).
FT   CONFLICT     117    117       S -> R (IN REF. 3).
FT   CONFLICT     129    129       R -> C (IN REF. 4).
SQ   SEQUENCE   239 AA;  26266 MW;  3C49F2B714DC9CCB CRC64;


  Query Match             40.5%;  Score 408.5;  DB 1;  Length 239;
  Best Local Similarity   36.6%;  Pred. No. 2.5e-29;
  Matches   86;  Conservative   35;  Mismatches   59;  Indels   55;  Gaps    5;

Qy       9 DTRALVADFVGYRLRQKGYVCGAG------------------PGE------------- 35
           | | :|  :: |:| |:||   ||                    ||
Db      10 DNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAPAPGIFSSQPGHTPHPAASRDPVART 69

Qy      36 ------------GPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQR 78
                       |||  |    :|  :| |||:|  |:|| |:::::|||:|| :|: |
Db      70 SPLQTPAAPGAAAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGR 129

Qy      79 FTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWI 138
           |  | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||
Db     130 FATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWI 189

Qy     139 HSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
             :|||  |  |||       | | : :| |::|:|: |: :|| :|:||:   |
Db     190 QDNGGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 239
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RESULT  14
BCL2_CRILO
ID   BCL2_CRILO     STANDARD;      PRT;   236 AA.
AC   Q9JJV8;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Apoptosis regulator Bcl-2.
GN   BCL2.
OS   Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Cricetulus.
OX   NCBI_TaxID=10030;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=20431763; PubMed=10973819;
RA   Tomicic M.T., Christmann M., Kaina B.;
RT   "Cloning and functional analysis of cDNA encoding the hamster Bcl-2
RT   protein.";
RL   Biochem. Biophys. Res. Commun. 275:899-903(2000).
RN   [2]
RP   SEQUENCE FROM N.A., AND CLEAVAGE BY CASPASES.
RX   MEDLINE=21092839; PubMed=11181062;
RA   Tomicic M.T., Kaina B.;
RT   "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9
RT   and caspase-3.";
RL   Biochem. Biophys. Res. Commun. 281:404-408(2001).
CC   -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC       including factor-dependent lymphohematopoietic and neural cells.
CC       Regulates cell death by controlling the mitochondrial membrane
CC       permeability. Appears to function in a feedback loop system with
CC       caspases. Inhibits caspase activity either by preventing the
CC       release of cytochrome c from the mitochondria and/or by binding to
CC       the apoptosis-activating factor (APAF-1) (By similarity).
CC   -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC       Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC       domains, and is necessary for anti-apoptotic activity (By
CC       similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC       membrane of the nuclear envelope and the endoplasmic reticulum.
CC   -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC       for interaction with RAF-1 (By similarity).
CC   -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC       anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC       on Ser-70 by PKC is required for the anti-apoptosis activity and
CC       occurs during the G2/M phase of the cell cycle (By similarity). In
CC       the absence of growth factors, Bcl2 appears to be phosphorylated
CC       by other protein kinases such as ERKs and stress-activated kinases
CC       (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A)
CC       (By similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC       cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC       activity, causes the release of cytochrome c into the cytosol
CC       promoting further caspase activity..
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AJ271720; CAB92245.1; -.
DR   HSSP; P53563; 1AF3.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
KW   Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
FT   DOMAIN       10     30       BH4.
FT   DOMAIN       90    104       BH3.
FT   DOMAIN      133    152       BH1.
FT   DOMAIN      184    199       BH2.
FT   TRANSMEM    209    230       POTENTIAL.
FT   SITE         64     65       CLEAVAGE (BY CASPASE-3 AND CASPASE-9).
FT   MOD_RES      70     70       PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
SQ   SEQUENCE   236 AA;  26491 MW;  BECADF1EF3337228 CRC64;

  Query Match             39.5%;  Score 399;  DB 1;  Length 236;
  Best Local Similarity   34.9%;  Pred. No. 1.7e-28;
  Matches   81;  Conservative   35;  Mismatches   64;  Indels   52;  Gaps    3;

Qy       9 DTRALVADFVGYRLRQKGY---------------------------------------- 27
           | | :|  :: |:| |:||
Db      10 DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART 69

Qy      28 ------VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                 |   ||   |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db      70 SPLRPIVATTGPTLSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
           | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||  :
Db     130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy     142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
           |||  |  |||       | | : :| |::|:|: |: :|| :|:| :   |
Db     190 GGWDAFVELYG----PSVRPLFDFSWLSLKTLLSLAL-VGACITLGTYLGHK 236


RESULT  15
AR11_XENLA
ID   AR11_XENLA     STANDARD;      PRT;   204 AA.
AC   Q91828;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Apoptosis regulator R11 (XR11).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Head;
RX   MEDLINE=95331613; PubMed=7607538;
RA   Cruz-Reyes J., Tata J.R.;
RT   "Cloning, characterization and expression of two Xenopus bcl-2-like
RT   cell-survival genes.";
RL   Gene 158:171-179(1995).
CC   -!- FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC   -!- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
CC       BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND
CC       ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC   -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
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CC   -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X82461; CAA57844.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR003093; BH4.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
KW   Apoptosis; Transmembrane.
FT   DOMAIN      101    120       BH1.
FT   DOMAIN      152    167       BH2.
FT   TRANSMEM    181    198       POTENTIAL.
SQ   SEQUENCE   204 AA;  23379 MW;  3BFC6BE6DDA4CA03 CRC64;


  Query Match             36.3%;  Score 366;  DB 1;  Length 204;
  Best Local Similarity   41.5%;  Pred. No. 1.2e-25;
  Matches   81;  Conservative   25;  Mismatches   63;  Indels   26;  Gaps    4;

Qy      10 TRALVADFVGYRLRQKGYVC----------------------GAGPGEGPAADPLHQAMR 47
           :| ||  ||  :| |    |                      | |  :|   : : ||:
Db       5 SRDLVEKFVSKKLSQ-NEACRKFSNNPNPMPYLMEPSTSERPGEGATQGIVEEEVLQALL 63

Qy      48 AAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALC 107
             | :||| |::| |||| :|||:|  :||| | ||  |||: | ||||:|||| || |||
Db      64 EATEEFELRYQRAFSDLTSQLHITQDTAQQSFQQVMGELFRDGTNWGRIVAFFSFGRALC 123

Qy     108 AESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLRE--G 165
           || ||||  |: ::  ||| |||  |  |:  :|||  |  |||  |  ::|  :|  |
Db     124 VESANKEMTDLLPRIVQWMVNYLEHTLQPWMQENGGWEAFVGLYGKNAAAQSRESQERFG 183

Qy     166 NWASVRTVLTGAVAL 180
             ::  :|||  ||
Db     184 RLLTI-VMLTGVFAL 197


Search completed: June 10, 2002, 10:32:13
Job time: 346 sec
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 10, 2002, 10:31:19 ; Search time 46.07 Seconds
(without alignments)
724.724 Million cell updates/sec

Title: US-09-155-327E-9
Perfect score: 1009
Sequence: 1 MATPASTPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1002	99.3	193	11	O88996	O88996 rattus norv
2	767	76.0	178	11	Q9CYW5	Q9cyw5 mus musculu
3	436.5	43.3	233	6	Q9MYW4	Q9myw4 oryctolagus
4	432.5	42.9	233	11	O35844	O35844 mus musculu
5	428.5	42.5	233	6	Q9N1A2	Q9n1a2 sus scrofa
6	425.5	42.2	233	6	Q9MZS7	Q9mzs7 ovis aries
7	401	39.7	180	6	Q9BDD5	Q9bdd5 bos taurus
8	401	39.7	217	11	Q99N35	Q99n35 mus musculu
9	399.5	39.6	180	6	Q9BDX7	Q9bdx7 bos taurus
10	397	39.3	238	13	Q90Z98	Q90z98 brachydanio
11	395	39.1	236	11	Q923R6	Q923r6 cricetulus
12	371.5	36.8	188	11	Q9QWX2	Q9qwx2 mus musculu
13	371.5	36.8	235	11	O35843	O35843 mus musculu
14	369.5	36.6	188	4	Q9H1R6	Q9h1r6 homo sapien
15	368	36.5	204	13	Q90ZH2	Q90zh2 xenopus lae
16	347	34.4	219	11	Q99N36	Q99n36 mus musculu
17	187	18.5	209	11	Q9JK59	Q9jk59 rattus norv
18	182	18.0	170	11	Q9WUI5	Q9wui5 rattus norv
19	177.5	17.6	192	13	Q9I9N4	Q9i9n4 brachydanio
20	175.5	17.4	221	13	Q98U13	Q98u13 xenopus lae
21	165.5	16.4	125	4	Q9H1R5	Q9h1r5 homo sapien
22	163	16.2	235	5	Q967D2	Q967d2 geodia cydo
23	162	16.1	58	11	Q9R1B3	Q9r1b3 rattus norv
24	157.5	15.6	163	6	Q9MZS6	Q9mzs6 ovis aries
25	154	15.3	173	11	Q9JKL3	Q9jk13 rattus norv
26	148.5	14.7	218	5	Q9N754	Q9n754 suberites d
27	147.5	14.6	179	4	Q9NYG7	Q9nyg7 homo sapien
28	145	14.4	149	6	Q9GMG7	Q9gmg7 ovis aries
29	144	14.3	177	13	Q90ZN1	Q90zn1 gallus gall
30	142	14.1	211	13	Q9W6F1	Q9w6f1 gallus gall
31	142	14.1	212	4	Q9UMX3	Q9umx3 homo sapien
32	141.5	14.0	179	12	Q9E1F2	Q9e1f2 meleagrid h
33	141	14.0	255	13	Q9I9N3	Q9i9n3 brachydanio
34	138.5	13.7	213	11	O35425	O35425 rattus norv
35	137.5	13.6	213	4	Q9UL32	Q9ul32 homo sapien
36	137.5	13.6	213	13	Q9I8I2	Q9i8i2 gallus gall
37	137.5	13.6	213	13	Q9DGJ5	Q9dgj5 gallus gall
38	136	13.5	114	4	Q9NR76	Q9nr76 homo sapien
39	130	12.9	162	12	Q9DH00	Q9dh00 meleagrid h
40	129.5	12.8	330	11	Q9Z1P3	Q9z1p3 rattus norv
41	127.5	12.6	331	11	P97287	P97287 mus musculu
42	124.5	12.3	91	11	Q923W5	Q923w5 peromyscus
43	121.5	12.0	91	11	Q923W6	Q923w6 peromyscus
44	121	12.0	174	13	Q9W6F2	Q9w6f2 gallus gall
45	119	11.8	300	5	Q9V9C8	Q9v9c8 drosophila

ALIGNMENTS

RESULT 1
O88996
ID O88996 PRELIMINARY; PRT; 193 AA.
AC O88996;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE BCL-W.
GN BCL-W.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE=99292146; PubMed=10366024;
RA Hamner S., Skoglosa Y., Lindholm D.;
RT "Differential expression of bcl-w and bcl-x messenger RNA in the
RT developing and adult rat nervous system.";
RL Neuroscience 91:673-684(1999).
DR EMBL; AF096291; AAC64200.1; -.
DR HSSP; Q07817; 1MAZ.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR000712; Bcl_2.
DR InterPro; IPR003093; BH4.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS50063; BH4_2; 1.
SQ SEQUENCE 193 AA; 20820 MW; 36D6742F4529AFB4 CRC64;

Query Match 99.3%; Score 1002; DB 11; Length 193;

```
  Best Local Similarity   99.0%;  Pred. No. 6.7e-80;
  Matches  191;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           ||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db       1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy     121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
           ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 QVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180

Qy     181 GALVTVGAFFASK 193
           |||||||||||||
Db     181 GALVTVGAFFASK 193


RESULT   2
Q9CYW5
ID   Q9CYW5      PRELIMINARY;      PRT;   178 AA.
AC   Q9CYW5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BCL2-LIKE 2.
GN   BCL2L2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK013244; BAB28740.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   MGD; MGI:108052; Bcl2l2.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   InterPro; IPR003093; BH4.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   178 AA;  19147 MW;  E2D4C3F79528E9D7 CRC64;

  Query Match             76.0%;  Score 767;  DB 11;  Length 178;
  Best Local Similarity   96.0%;  Pred. No. 2e-59;
  Matches  144;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
           ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db       1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

Qy      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120

Qy     121 QVQDWMVAYLETRLADWIHSSGGWAEFTAL 150
           |||||||||||||||||||||||||   : |
Db     121 QVQDWMVAYLETRLADWIHSSGGWVRSSQL 150


RESULT   3
Q9MYW4
ID   Q9MYW4      PRELIMINARY;      PRT;   233 AA.
AC   Q9MYW4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   BCL-X.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Knott J.C., Robertson L., James E.R.;
RT   "Rabbit Bcl-X.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY005131; AAF88137.1; -.
DR   HSSP; P53563; 1AF3.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   InterPro; IPR003093; BH4.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   233 AA;  25986 MW;  12F0F30344D53F93 CRC64;

  Query Match             43.3%;  Score 436.5;  DB 6;  Length 233;
  Best Local Similarity   41.5%;  Pred. No. 2e-30;
  Matches   93;  Conservative   23;  Mismatches   57;  Indels   51;  Gaps    4;

Qy      11 RALVADFVGYRLRQKGYVC--------------GAG---------------PGEGPAA 39
           | || ||: |:| ||||                 | |               | : ||
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTGPEMETPSAINGNPAWHPADSPAV 65

Qy      40 D-----------------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
           :                 : ||:| |||||| |:|| |||| :|||:|||:| | | |
Db      66 NGATGHSSSLDAREVIPMTAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 125

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
           | :|||: | ||||:|||| || ||| |||:|||| || ::  ||  ||   |  ||  :
Db     126 VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMEVLVSRIAAWMATYLNDHLEPWIQEN 185

Qy     142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           |||  |  |||: |  |:|: :|    |      : | | ||:|
Db     186 GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229
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```
RESULT   4
O35844
ID   O35844      PRELIMINARY;      PRT;   233 AA.
AC   O35844;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BCL-XL.
GN   BCL2L.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B6/CBA; TISSUE=THYMUS;
RX   MEDLINE=98051053; PubMed=9390687;
RA   Yang X.-F., Weber G.F., Cantor H.;
RT   "A novel Bcl-x isoform connected to the T cell receptor regulates
RT   apoptosis in T cells.";
RL   Immunity 7:629-639(1997).
DR   EMBL; U51278; AAC53459.1; -.
DR   HSSP; P53563; 1AF3.
DR   MGD; MGI:88139; Bcl2l.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   InterPro; IPR003093; BH4.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   233 AA;  26033 MW;  3083F2D8327E072E CRC64;


  Query Match             42.9%;  Score 432.5;  DB 11;  Length 233;
  Best Local Similarity   41.3%;  Pred. No. 4.4e-30;
  Matches   93;  Conservative   23;  Mismatches   56;  Indels   53;  Gaps    4;

Qy      11 RALVADFVGYRLRQKGY----------------------------------------V 28
           | || ||: |:| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy     141 SGGWAEFTALYGDGALEEARRLREG--NWASVRTVLTGAVALGAL 183
           :|||  |  |||: |  |:|: :||   |      : | | ||:|
Db     185 NGGWDTFVDLYGNNAAAESRKGKEGFNRWFLTGMTVAGVVLLGSL 229


RESULT   5
Q9N1A2
ID   Q9N1A2      PRELIMINARY;      PRT;   233 AA.
AC   Q9N1A2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANTI-APOPTOTIC REGULATOR BCL-XL.
GN   BCL-XL.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART;
RA   Lee T.L., Canty J.M.;
RT   "PCR Cloning of a Porcine bcl-xL cDNA from Heart.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF216205; AAF33212.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   InterPro; IPR003093; BH4.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   233 AA;  26047 MW;  2FA312818B25E17D CRC64;


  Query Match             42.5%;  Score 428.5;  DB 6;  Length 233;
  Best Local Similarity   41.3%;  Pred. No. 9.9e-30;
  Matches   93;  Conservative   22;  Mismatches   57;  Indels   53;  Gaps    4;

Qy      11 RALVADFVGYRLRQKGY----------------------------------------V 28
           | || ||: |:| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQE 184

Qy     141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           :|||  |  |||: |  |:|: :|   |      | | | ||:|
Db     185 NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTLAGVVLLGSL 229


RESULT   6
Q9MZS7
ID   Q9MZS7      PRELIMINARY;      PRT;   233 AA.
AC   Q9MZS7;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   BCL-X LONG PROTEIN.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=OVARY;
RA   Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;
RT   "Bcl-x in the sheep ovary.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF164517; AAF89532.1; -.
DR   HSSP; P53563; 1AF3.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   InterPro; IPR003093; BH4.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
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DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   233 AA;  26134 MW;  012BFA1382762915 CRC64;


  Query Match             42.2%;  Score 425.5;  DB 6;  Length 233;
  Best Local Similarity   40.2%;  Pred. No. 1.8e-29;
  Matches   90;  Conservative   24;  Mismatches   59;  Indels   51;  Gaps    4;

Qy      11 RALVADFVGYRLRQKGY----------------------------VCGAGP----GEGPAA 39
           | || ||: |:| ||||                             |     : ||
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESDMETPSAINGNPSWHLADSPAV 65

Qy      40 D------------------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
           :                  : ||:| |||||| |:|| |||| :|||:|||:| | | |
Db      66 NGATGHSRSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 125

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
           | :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||  :
Db     126 VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQEN 185

Qy     142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
           |||  |  |||: |  |:|: :|    |      : | | ||:|
Db     186 GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229


RESULT   7
Q9BDD5
ID   Q9BDD5      PRELIMINARY;      PRT;   180 AA.
AC   Q9BDD5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANTI-APOPTOTIC REGULATOR BCL-XL (FRAGMENT).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Amills M., Bouzat J.;
RT   "Characterization of the bovine bcl-xL gene and related pseudogenes.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF245488; AAK31307.1; -.
DR   EMBL; AF245489; AAK31308.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   SMART; SM00337; BCL; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
FT   NON_TER       1      1
FT   NON_TER     180    180
SQ   SEQUENCE   180 AA;  20062 MW;  95DC436F95DABDA6 CRC64;


  Query Match             39.7%;  Score 401;  DB 6;  Length 180;
  Best Local Similarity   53.5%;  Pred. No. 1.8e-27;
  Matches   76;  Conservative   19;  Mismatches   45;  Indels    2;  Gaps    1;

Qy      44 QAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFG 103
           ||:| |||||| |:|| |||| :|||:|||:| | | || :|||: | ||||:|||| ||
Db      38 QALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFG 97

Qy     104 AALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLR 163
           ||| |||:|||: || ::  ||  ||   |  ||  :|||  |  |||: |  |:|: :
Db      98 GALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQ 157

Qy     164 E--GNWASVRTVLTGAVALGAL 183
           |    |      : | | ||:|
Db     158 ERFNRWFLTGMTVAGVVLLGSL 179


RESULT   8
Q99N35
ID   Q99N35      PRELIMINARY;      PRT;   217 AA.
AC   Q99N35;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   B-CELL LEUKEMIA/LYMPHOMA X (FRAGMENT).
GN   BCLX.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SVJ;
RA   Yang X.-F., Cantor H.;
RT   "Novel cDNA structure and genomic organization of apoptosis regulatory
RT   gene Bcl-x-gamma.";
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF133282; AAK15455.1; -.
DR   EMBL; AF133281; AAK15455.1; JOINED.
DR   HSSP; P53563; 1AF3.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   SMART; SM00337; BCL; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   217 AA;  24234 MW;  3B5A4E809A7DEF18 CRC64;


  Query Match             39.7%;  Score 401;  DB 11;  Length 217;
  Best Local Similarity   53.5%;  Pred. No. 2.3e-27;
  Matches   76;  Conservative   19;  Mismatches   45;  Indels    2;  Gaps    1;

Qy      44 QAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFG 103
           ||:| |||||| |:|| |||| :|||:|||:| | | || :|||: | ||||:|||| ||
Db      72 QALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFG 131

Qy     104 AALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLR 163
           ||| |||:|||: || ::  ||  ||   |  ||  :|||  |  |||: |  |:|: :
Db     132 GALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENGGWDTFVDLYGNNAAAESRKGQ 191

Qy     164 E--GNWASVRTVLTGAVALGAL 183
           |    |      : | | ||:|
Db     192 ERFNRWFLTGMTVAGVVLLGSL 213


RESULT   9
Q9BDX7
ID   Q9BDX7      PRELIMINARY;      PRT;   180 AA.
AC   Q9BDX7;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ANTI-APOPTOTIC REGULATOR BCL-XL (FRAGMENT).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
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OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Amills M., Bouzat J.;
RT   "Characterization of the bovine bcl-xL gene and related pseudogenes.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF245487; AAK31306.1; -.
DR   HSSP; Q07817; 1MAZ.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   Pfam; PF00452; Bcl-2; 1.
DR   SMART; SM00337; BCL; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01258; BH2; 1.
DR   PROSITE; PS01259; BH3; 1.
FT   NON_TER       1       1
FT   NON_TER     180     180
SQ   SEQUENCE   180 AA;  20056 MW;  62C4C0BD0555A9EF CRC64;


  Query Match             39.6%;  Score 399.5;  DB 6;  Length 180;
  Best Local Similarity   47.1%;  Pred. No. 2.4e-27;
  Matches   82;  Conservative   23;  Mismatches   58;  Indels   11;  Gaps    3;

Qy      20 YRLRQKGYVCGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVT 71
           : |      | || ||   ::|         : ||:| |||||| |:|| |||| :|||:|
Db       7 WHLEDSPAVNGA-PGHSRSSDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHIT 65

Qy      72 PGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLE 131
           ||:| | | || :|||: | ||||:|| | || ||| |||:|||: || ::  ||  ||
Db      66 PGTAYQSFEQVVNELFRDGVNWGRIVASFSFGGALCVESVDKEMQVLVSRIATWMATYLN 125

Qy     132 TRLADWIHSSGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
             |  ||  :|||  |  |||: |  |:|: :|    |       : | | ||:|
Db     126 DHLEPWIQENGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 179


RESULT  10
Q90Z98
ID   Q90Z98      PRELIMINARY;      PRT;   238 AA.
AC   Q90Z98;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BCL-XL-LIKE PROTEIN 1.
GN   BLP1.
OS   Brachydanio rerio (Zebrafish) (Zebra danio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21299061; PubMed=11406282;
RA   Chen M.-C., Gong H.-Y., Cheng C., Wang J.-P., Hong J., Wu J.-L.;
RT   "Cloning and characterization of zfBLP1, a Bcl-XL homologue from the
RT   zebrafish, Danio rerio(1).";
RL   Biochim. Biophys. Acta 1519:127-133(2001).
DR   EMBL; AF317837; AAK81706.1; -.
SQ   SEQUENCE   238 AA;  26253 MW;  6E58394933EEFDDB CRC64;


  Query Match             39.3%;  Score 397;  DB 13;  Length 238;
  Best Local Similarity   35.7%;  Pred. No. 5.7e-27;
  Matches   85;  Conservative   29;  Mismatches   62;  Indels   62;  Gaps    6;

Qy      11 RALVADFVGYRLRQKGYVC------------------GAG-------------------- 32
           | ||  |: |:| |: | |                   | |
Db       6 RELVVFFIKYKLSQRNYPCNHIGLTEDTNRTDGAEENGEGAAGATTLVNGTMNRTNASST 65

Qy      33 --PGEGPAADPLHQ------------AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQR 78
             | : ||: |  |             |:| : :||| |: | |:||::|||:|| :| |
Db      66 GTPPQSPASSPQRQTNGSGGLDAVKEALRDSANEFELRYSRAFNDLSSQLHITPATAYQS 125

Qy      79 FTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWI 138
           |  | ||:|: | ||||:|  | || ||| | | ||| ||||:: :|| ||:  :  ||
Db     126 FESVMDEVFRDGVNWGRIVGLFAFGGALCVECVEKEMSPLVGRIAEWMTVYLDNHIQPWI 185

Qy     139 HSSGGWAEFTALYGDGALEEARRLREG--NWA-SVRTVLTGAVALGALVTVGAFFASK 193
             | |||  |  ::|  |  |:|: :|    |  :  |:|||       | ||   | |
Db     186 QSQGGWERFAEIFGKDAAAESRKSQESFKKWLFAGMTLLTG-------VVVGGLIAQK 236


RESULT  11
Q923R6
ID   Q923R6      PRELIMINARY;      PRT;   236 AA.
AC   Q923R6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   B-CELL LYMPHOMA PROTEIN 2.
GN   BCL2.
OS   Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Cricetulus.
OX   NCBI_TaxID=10030;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lai D.Z., Chen W., Wang H.T.;
RT   "Construction of a robust CHO cell line for biopharmaceutical use.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF404339; AAK92201.1; -.
SQ   SEQUENCE   236 AA;  26500 MW;  BEDF052EF32CA8B8 CRC64;


  Query Match             39.1%;  Score 395;  DB 11;  Length 236;
  Best Local Similarity   34.9%;  Pred. No. 8.5e-27;
  Matches   81;  Conservative   33;  Mismatches   66;  Indels   52;  Gaps    3;

Qy       9 DTRALVADFVGYRLRQKGY---------------------------------------- 27
           | | :|  :: |:| |:||
Db      10 DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART 69

Qy      28 ------VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                 |   ||   |    :|  :| |||:|  |:|| |:::::|||:|| :|: ||
Db      70 SPLRPIVATTGPTLSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129

Qy      82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
           | :|||: | ||||:|||| ||  :| ||||:|| |||  :  ||  ||   |  ||  :
Db     130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189

Qy     142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
           |||  |  |||       | | : :| |: |:|  |: :|| :|:| :   |
Db     190 GGWDAFVELYG----PSVRPLFDFSWLSLXTLLNLAL-VGACITLGTYLGHK 236


RESULT  12
Q9QWX2
ID   Q9QWX2      PRELIMINARY;      PRT;   188 AA.
AC   Q9QWX2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BCL-X (FRAGMENT).
GN   BCL2L.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20350651; PubMed=10894153;
RA   Rucker E.B. III, Dierisseau P., Wagner K.U., Garrett L.,
RA   Wynshaw-Boris A., Flaws J.A., Hennighausen L.;
RT   "Bcl-x and Bax regulate mouse primordial germ cell survival and
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RT   apoptosis during embryogenesis.";
RL   Mol. Endocrinol. 14:1038-1052(2000).
DR   EMBL; AF088904; AAC72232.1; -.
DR   HSSP; P53563; 1AF3.
DR   MGD; MGI:88139; Bcl2l.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   InterPro; IPR003093; BH4.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
FT   NON_TER     188    188
SQ   SEQUENCE   188 AA;  21126 MW;  4E62F8356D248E52 CRC64;


  Query Match             36.8%;  Score 371.5;  DB 11;  Length 188;
  Best Local Similarity   42.4%;  Pred. No. 7.1e-25;
  Matches   78;  Conservative   17;  Mismatches   38;  Indels   51;  Gaps    3;

Qy      11 RALVADFVGYRLRQKGY----------------------------------------V 28
           | || ||: |:| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy     141 SGGW 144
           :|||
Db     185 NGGW 188


RESULT  13
O35843
ID   O35843      PRELIMINARY;      PRT;   235 AA.
AC   O35843;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BCL-X-GAMMA.
GN   BCL2L.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B6/CBA; TISSUE=THYMUS;
RX   MEDLINE=98051053; PubMed=9390687;
RA   Yang X.-F., Weber G.F., Cantor H.;
RT   "A novel Bcl-x isoform connected to the T cell receptor regulates
RT   apoptosis in T cells.";
RL   Immunity 7:629-639(1997).
DR   EMBL; U51277; AAC53458.1; -.
DR   HSSP; P53563; 1AF3.
DR   MGD; MGI:88139; Bcl2l.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   InterPro; IPR003093; BH4.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS01259; BH3; 1.
DR   PROSITE; PS01260; BH4_1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
SQ   SEQUENCE   235 AA;  26122 MW;  649D914C2D5378F6 CRC64;


  Query Match             36.8%;  Score 371.5;  DB 11;  Length 235;
  Best Local Similarity   42.4%;  Pred. No. 9.5e-25;
  Matches   78;  Conservative   17;  Mismatches   38;  Indels   51;  Gaps    3;

Qy      11 RALVADFVGYRLRQKGY----------------------------------------V 28
           | || ||: |:| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184

Qy     141 SGGW 144
           :|||
Db     185 NGGW 188


RESULT  14
Q9H1R6
ID   Q9H1R6      PRELIMINARY;      PRT;   188 AA.
AC   Q9H1R6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BA243J16.1.1 (BCL2-LIKE 1 (ISOFORM 1)) (FRAGMENT).
GN   BCL2L1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Brown A.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL160175; CAC10003.1; -.
DR   HSSP; Q07817; 1LXL.
DR   InterPro; IPR002475; BCL2_family.
DR   InterPro; IPR000712; Bcl_2.
DR   InterPro; IPR003093; BH4.
DR   Pfam; PF00452; Bcl-2; 1.
DR   Pfam; PF02180; BH4; 1.
DR   SMART; SM00337; BCL; 1.
DR   SMART; SM00265; BH4; 1.
DR   PROSITE; PS50062; BCL2_FAMILY; 1.
DR   PROSITE; PS01080; BH1; 1.
DR   PROSITE; PS50063; BH4_2; 1.
FT   NON_TER     188    188
SQ   SEQUENCE   188 AA;  21029 MW;  7074B6095145C324 CRC64;


  Query Match             36.6%;  Score 369.5;  DB 4;  Length 188;
  Best Local Similarity   42.4%;  Pred. No. 1.1e-24;
  Matches   78;  Conservative   17;  Mismatches   38;  Indels   51;  Gaps    3;

Qy      11 RALVADFVGYRLRQKGY----------------------------------------V 28
           | || ||: |:| ||||                                        |
Db       6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65

Qy      29 CGAGPGEGPAAD--------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
             ||  |   : |         : ||:| |||||| |:|| |||| :|||:|||:| | |
Db      66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
```

```
Qy      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
           || :|||: | ||||:|||| || ||| |||:|||: || ::  ||  ||   |  ||
Db     125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE 184

Qy     141 SGGW 144
           :|||
Db     185 NGGW 188
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RESULT 15
Q90ZH2
ID Q90ZH2 PRELIMINARY; PRT; 204 AA.
AC Q90ZH2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE BCL-XL.
GN BCL-XL.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakajima K., Yaoita Y.;
RT "Muscle cell death occurs in the regressing tail of tadpole by a
RT suicide mechanism.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB055494; BAB62748.1; -.
SQ SEQUENCE 204 AA; 23189 MW; 1BEF1B904E29D84A CRC64;

Query Match 36.5%; Score 368; DB 13; Length 204;
Best Local Similarity 42.3%; Pred. No. 1.6e-24;
Matches 82; Conservative 24; Mismatches 64; Indels 24; Gaps 4;

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Qy      10 TRALVADFVGYRLRQ----------------KGYVCGAGPGEGP----AADPLHQAMRA 48
           :| ||  ||  :| |                |     ||||      : : ||:
Db       5 SRDLVEKFVSKKLSQNEACRKFSNNPQPNAISNGTSTSERPGEGATQGIVEEEVLQALLE 64

Qy      49 AGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCA 108
           | :||| |::| |||| :|||:|  :||| | ||  |||: | ||||:|||| || |||
Db      65 ATEEFELRYQRAFSDLTSQLHITQDTAQQSFQQVMGELFRDGTNWGRIVAFFSFGRALCV 124

Qy     109 ESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLRE--GN 166
           || ||||  |: ::  ||| |||  |  |:  :|||  |  |||  |  ::|  :|  |
Db     125 ESANKEMTDLLPRIVQWMVNYLEHTLQPWMQENGGWEAFVGLYGKNAAAQSRESQERFGR 184

Qy     167 WASVRTVLTGAVAL 180
             ::  :|||  ||
Db     185 LLTI-VMLTGVFAL 197
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Search completed: June 10, 2002, 10:31:19
Job time: 392 sec